

## SEQUENCE LISTING

- <110> Genentech, Inc.  
Ashkenazi, Avi  
Botstein, David  
Desnoyers, Luc  
Eaton, Dan L.  
Ferrara, Napoleone  
Filvaroff, Ellen  
Fong, Sherman  
Gao, Wei-Qiang  
Gerber, Hanspeter  
Gerritsen, Mary E.  
Goddard, A.  
Godowski, Paul J.  
Grimaldi, Christopher J.  
Gurney, Austin L.  
Hillan, Kenneth, J.  
Kljavin, Ivar J.  
Mather, Jennie P.  
Pan, James  
Paoni, Nicholas F.  
Roy, Margaret Ann  
Stewart, Timothy A.  
Tumas, Daniel  
Williams, P. Mickey  
Wood, William, I.
- <120> Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same
- <130> 10466-14
- <140> 09/665,350  
<141> 2000-09-18
- <150> PCT/US00/04414  
<151> 2000-02-22
- <150> US 60/143,048  
<151> 1999-07-07
- <150> US 60/145,698  
<151> 1999-07-26
- <150> US 60/146,222  
<151> 1999-07-28
- <150> PCT/US99/20594  
<151> 1999-09-08
- <150> PCT/US99/20944  
<151> 1999-09-13

T03T20"02E60660

<150> PCT/US99/21090  
<151> 1999-09-15

<150> PCT/US99/21547  
<151> 1999-09-15

<150> PCT/US99/23089  
<151> 1999-10-05

<150> PCT/US99/28214  
<151> 1999-11-29

<150> PCT/US99/28313  
<151> 1999-11-30

<150> PCT/US99/28564  
<151> 1999-12-02

<150> PCT/US99/28565  
<151> 1999-12-02

<150> PCT/US99/30095  
<151> 1999-12-16

<150> PCT/US99/30911  
<151> 1999-12-20

<150> PCT/US99/30999  
<151> 1999-12-20  
<150> PCT/US00/00219  
<151> 2000-01-05

<160> 423

<210> 1  
<211> 1825  
<212> DNA  
<213> Homo sapiens

<400> 1  
actgcacctc gggttctatcg attgaattcc ccgggggatcc tctagagatc cctcgacctc 60  
gacccacgcg tccggggccgg agcagcacgg ccgcaggacc tggagctccg gctgcgtctt 120  
cccgcagcgc taccgcgccat gcgcctgccg ccgcggggccg cgctggggct cctgccgctt 180  
ctgctgctgc tgcgcgccgc gccggaggcc gccaaagaagc cgacgcctcg ccaccgggtgc 240  
cggggggctgg tggacaagtt taaccagggg atggtggaca ccgcaaagaa gaactttggc 300  
ggcgggaaca cggcttggga ggaaaagacg ctgtccaagt acgagtccag cgagattcgc 360  
ctgctggaga tcctggaggg gctgtgcgag agcagcgact tcgaatgcaa tcagatgcta 420  
gaggcgcagg aggagcacct ggaggcctgg tggctgcagc tgaagagcga atatcctgac 480  
ttattcgagt ggttttgtgt gaagacactg aaagtgtgct gctctccagg aacctacggt 540  
cccgactgtc tcgcatgcca gggcgggatcc cagaggccct gcagcgggaa tggccactgc 600  
agcggagatg ggagcagaca gggcgacggg tcctgccggt gccacatggg gtaccagggc 660

ccgctgtgca ctgactgcat ggacggctac ttcagctcgc tccggaacga gacccacagc 720  
 atctgcacag cctgtgacga gtcctgcaag acgtgctcgg gcctgaccaa cagagactgc 780  
 ggcgagtgtg aagtgggctg ggtgctggac gagggcgctt gtgtggatgt ggacgagtgt 840  
 gcggccgagc cgcctccctg cagcgtgctg cagttctgta agaacgcaa cggctcctac 900  
 acgtgcgaag agtgtgactc cagctgtgtg ggctgcacag gggaaggccc aggaaactgt 960  
 aaagagtgtg tctctggcta cgcgaggag cagcgacagt gtgcagatgt ggacgagtgc 1020  
 tctactagcag aaaaaacctg tgtgaggaaa aacgaaaact gctacaatac tccagggagc 1080  
 tacgtctgtg tgtgtcctga cggcttcgaa gaaacggaag atgcctgtgt gccgccggca 1140  
 gaggtgaag ccacagaagg agaaagccc acacagctgc cctcccgcga agacctgtaa 1200  
 tgtgccggac ttacccttta aattattcag aaggatgtcc cgtggaaaat gtggccctga 1260  
 ggatgccgtc tctgacagt gacagcggcg gggagaggct gcctgtcttc taacggttga 1320  
 ttctcatttg tcccttaaac agctgcattt cttggttgtt cttaaacaga cttgtatatt 1380  
 ttgatacagt tctttgtaat aaaattgacc attgtaggta atcaggagga aaaaaaaaaa 1440  
 aaaaaaaaaa aaagggcggc cgcgactcta gagtcgacct gcagaagctt ggccgccatg 1500  
 gcccaacttg tttattgcag cttataatgg ttacaaataa agcaatagca tcacaaattt 1560  
 cacaaataaa gcatTTTTTT cactgcattc tagttgtggt ttgtccaaac tcatcaatgt 1620  
 atcttatcat gtctggatcg ggaattaatt cggcgacgca ccatggcctg aaataacctc 1680  
 tgaaagagga acttggttag gtaccttctg aggcggaaaag aaccagctgt ggaatgtgtg 1740  
 tcagttaggg tgtggaaagt ccccaggctc cccagcaggc agaagtatgc aagcatgcat 1800  
 ctcaattagt cagcaaccca gtttt 1825

<210> 2

<211> 353

<212> PRT

<213> Homo sapiens

<400> 2

Met Arg Leu Pro Arg Arg Ala Ala Leu Gly Leu Leu Pro Leu Leu Leu  
 1 5 10 15  
 Leu Leu Pro Pro Ala Pro Glu Ala Ala Lys Lys Pro Thr Pro Cys His  
 20 25 30  
 Arg Cys Arg Gly Leu Val Asp Lys Phe Asn Gln Gly Met Val Asp Thr  
 35 40 45  
 Ala Lys Lys Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Lys Thr  
 50 55 60  
 Leu Ser Lys Tyr Glu Ser Ser Glu Ile Arg Leu Leu Glu Ile Leu Glu  
 65 70 75 80  
 Gly Leu Cys Glu Ser Ser Asp Phe Glu Cys Asn Gln Met Leu Glu Ala  
 85 90 95  
 Gln Glu Glu His Leu Glu Ala Trp Trp Leu Gln Leu Lys Ser Glu Tyr  
 100 105 110  
 Pro Asp Leu Phe Glu Trp Phe Cys Val Lys Thr Leu Lys Val Cys Cys  
 115 120 125  
 Ser Pro Gly Thr Tyr Gly Pro Asp Cys Leu Ala Cys Gln Gly Gly Ser  
 130 135 140

09909320-071801

```
<400> 3
cagggtccaac tgcacctcgg ttctatcgat tgaattcccc ggggatcctc tagagatccc 60
tcgacctcga cccacgcgctc cgccaggccg ggaggcgacg cgcccagccg tctaaacggg 120
aacagccctg gctgaggggag ctgcagcgca gcagagtatc tgacggcgcc aggttgcgta 180
ggtgcggcac gaggagtttt cccggcagcg aggaggtcct gaggcagcatg gcccgaggga 240
```

gcgccttccc tgccgcgcgc ctctggctct ggagcatcct cctgtgcctg ctggcactgc 300  
 gggcggaggc cgggcccgcg caggaggaga gcctgtacct atggatcgat gctcaccagg 360  
 caagagtact cataggattt gaagaagata tcctgattgt ttcagagggg aaaatggcac 420  
 cttttacaca tgatttcaga aaagcgcaac agagaatgcc agctattcct gtcaatatcc 480  
 attccatgaa ttttacctgg caagctgcag ggcaggcaga atacttctat gaattcctgt 540  
 ccttgcgctc cctggataaa ggcatcatgg cagatccaac cgtcaatgtc cctctgctgg 600  
 gaacagtgcc tcacaaggca tcagttgttc aagttggttt cccatgtctt ggaaaacagg 660  
 atgggggtggc agcatttgaa gtggatgtga ttgttatgaa ttctgaaggc aacaccattc 720  
 tccaaacacc tcaaaatgct atcttcttta aaacatgtca acaagctgag tgcccaggcg 780  
 ggtgccgaaa tggaggcttt tgtaatgaaa gacgcatctg cgagtgtcct gatgggttcc 840  
 acggacctca ctgtgagaaa gccctttgta cccacgatg tatgaatggg ggactttgtg 900  
 tgactcctgg tttctgcatc tgcccacctg gattctatgg agtgaactgt gacaaagcaa 960  
 actgctcaac cacctgcttt aatggaggga cctgtttcta cctggaaaa tgtatttgcc 1020  
 ctccaggact agaggggagag cagtgtgaaa tcagcaaatg cccacaacc tgtcgaaatg 1080  
 gaggtaaatg cattggtaaa agcaaatgta agtgttccaa aggttaccag ggagacctct 1140  
 gttcaaagcc tgtctgcgag cctggctgtg gtgcacatgg aacctgccat gaacccaaca 1200  
 aatgccaatg tcaagaagg tggcatggaa gacactgcaa taaaaggtag gaagccagcc 1260  
 tcatacatgc cctgaggcca gcaggcgccc agctcaggca gcacacgct tcacttaaaa 1320  
 agggcgagga gcggcgggat ccacctgaat ccaattacat ctggtgaact ccgacatctg 1380  
 aaacgtttta agttacacca agttcatagc ctttgttaac ctttcatgtg ttgaatgttc 1440  
 aaataatggt cattacactt aagaatactg gcctgaattt tattagcttc attataaatc 1500  
 actgagctga tatttactct tccttttaag ttttctaagt acgtctgtag catgatggta 1560  
 tagattttct tgtttcagtg ctttgggaca gattttatat tatgtcaatt gatcagggtta 1620  
 aaattttcag tgtgtagttg gcagatattt tcaaaattac aatgcattta tgggtgtctgg 1680  
 gggcagggga acatcagaaa ggttaaattg ggcaaaaatg cgtaagtcac aagaatttgg 1740  
 atggtgcagt taatgttgaa gttacagcat ttcagatttt attgtcagat atttagatgt 1800  
 ttgttacatt tttaaaaatt gctcttaatt tttaaactct caatacaata tattttgacc 1860  
 ttaccattat tccagagatt cagtattaaa aaaaaaaaaa ttactgtg gtagtggcat 1920  
 ttaacaata taatatattc taaacacaat gaaataggga atataatgta tgaacttttt 1980  
 gcattggctt gaagcaatat aatatattgt aaacaaaaca cagctcttac ctaataaaca 2040  
 ttttatactg tttgtatgta taaaataaag gtgctgcttt agttttttgg aaaaaaaaaa 2100  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa gggcggccgc gactctagag tcgacctgca 2160  
 gaagcttggc cgccatggcc caacttgttt attgcagctt ataatg 2206

<210> 4  
 <211> 379  
 <212> PRT  
 <213> Homo sapiens

<400> 4  
 Met Ala Arg Arg Ser Ala Phe Pro Ala Ala Ala Leu Trp Leu Trp Ser  
 1 5 10 15  
 Ile Leu Leu Cys Leu Leu Ala Leu Arg Ala Glu Ala Gly Pro Pro Gln  
 20 25 30  
 Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu  
 35 40 45  
 Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala  
 50 55 60  
 Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile

65		70		75		80
Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln						
	85			90		95
Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly						
	100			105		110
Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro						
	115			120		125
His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln						
	130			135		140
Asp Gly Val Ala Ala Phe Glu Val Asp Val Ile Val Met Asn Ser Glu						
	145			150		155
Gly Asn Thr Ile Leu Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr						
	165			170		175
Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys						
	180			185		190
Asn Glu Arg Arg Ile Cys Glu Cys Pro Asp Gly Phe His Gly Pro His						
	195			200		205
Cys Glu Lys Ala Leu Cys Thr Pro Arg Cys Met Asn Gly Gly Leu Cys						
	210			215		220
Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn						
	225			230		235
Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys						
	245			250		255
Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln						
	260			265		270
Cys Glu Ile Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys						
	275			280		285
Ile Gly Lys Ser Lys Cys Lys Cys Ser Lys Gly Tyr Gln Gly Asp Leu						
	290			295		300
Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys						
	305			310		315
His Glu Pro Asn Lys Cys Gln Cys Gln Glu Gly Trp His Gly Arg His						
	325			330		335
Cys Asn Lys Arg Tyr Glu Ala Ser Leu Ile His Ala Leu Arg Pro Ala						
	340			345		350

09909320-071801



<210> 9  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 9  
 aaagacgcat ctgcgagtgt cc 22

<210> 10  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 10  
 tgctgatttc aactgctct ccc 23

<210> 11  
 <211> 2197  
 <212> DNA  
 <213> Homo sapiens

<400> 11  
 cggacgcgtg ggcgtccggc ggtcgcagag ccaggaggcg gaggcgcgcg ggccagcctg 60  
 ggccccagcc cacaccttca ccaggggccca ggagccacca tgtggcgatg tccactgggg 120  
 ctactgctgt tgcgtccgct ggctggccac ttggctcttg gtgccagca gggtcgtggg 180  
 cgccgggagc tagcaccggg tctgcacctg cggggcatcc gggacgcggg aggcgcgtac 240  
 tgccaggagc aggacctgtg ctgccgcggc cgtgccgacg actgtgccct gccctacctg 300  
 ggcgccatct gttactgtga cctcttctgc aaccgcacgg tctccgactg ctgccctgac 360  
 ttctgggact tctgcctcgg cgtgccaccc ccttttcccc cgatccaagg atgtatgcat 420  
 ggaggtcgta tctatccagt cttgggaacg tactgggaca actgtaaccg ttgcacctgc 480  
 caggagaaca ggcagtggca tgggtggatcc agacatgatc aaagccatca accagggcaa 540  
 ctatggctgg caggtcggga accacagcgc cttctggggc atgaccctgg atgagggcat 600  
 tcgtaccgc ctgggcacca tccgcccatc ttctcgggtc atgaacatgc atgaaattta 660  
 tacagtgctg aaccacgggg aggtgcttcc cacagccttc gaggcctctg agaagtggcc 720  
 caacctgatt catgagcctc ttgaccaagg caactgtgca ggctcctggg ccttctccac 780  
 agcagctgtg gcatccgacg gtgtctcaat ccattctctg ggacacatga cgctgtcctc 840  
 gtcgccccag aacctgctgt cttgtgacac ccaccagcag cagggtgcc gcggtgggag 900  
 tctcgatggg cctgggtggg tctcgctcgc ccgaggggtg gtgtctgacc actgctaccc 960  
 cttctcgggc cgtgaacgag acgaggctgg ccctgcgccc ccctgtatga tgcacagccg 1020  
 agccatgggt cggggcaagc gccaggccac tgcccactgc cccaacagct atgttaataa 1080  
 caatgacatc taccaggtca ctctgtcta ccgctcggc tccaacgaca aggagatcat 1140  
 gaaggagctg atggagaatg gccctgtcca agccctcatg gaggtgcatg aggacttctt 1200  
 cctatacaag ggaggcatct acagccacac gccagtgagc cttgggaggc cagagagata 1260  
 ccgcccggcat gggacccact cagtcaagat cacaggatgg ggagaggaga cgctgccaga 1320



```

tgaaggacg ctcaaatact ggactgcggc caactcctgg ggcccagcct ggggcgagag 1380
gggccacttc cgcctcgtgc gcggcgtaa tgagtgcgac atcgagagct tcgtgctggg 1440
cgtctggggc cgcgtgggca tggaggacat gggcatcac tgaggctgcg ggcaccacgc 1500
ggggtccggc ctgggatcca ggctaagggc cggcggaaga ggccccaatg gggcggtgac 1560
cccagcctcg cccgacagag cccggggcgc aggcgggcgc cagggcgcta atcccggcgc 1620
gggttccgct gacgcagcgc cccgcctggg agccgcgggc aggcgagact ggcggagccc 1680
ccagacctcc cagtggggac ggggcagggc ctggcctggg aagagcacag ctgcagatcc 1740
caggcctctg gcgccccac tcaagactac caaagccagg acacctcaag tctccagccc 1800
caatacccca cccaatccc gtattctttt ttttttttt ttagacaggg tcttgctccg 1860
ttgcccaggt tggagtgcag tggcccatca gggctcactg taacctccga ctctggggtt 1920
caagtgacct tcccacctca gcctctcaag tagctgggac tacagggtgca ccaccacacc 1980
tggctaattt ttgtatttt tgtaaagagg ggggtctcac tgtgttgccc aggctgggtt 2040
cgaactcctg ggctcaagcg gtccacctgc ctccgcctcc caaagtgcgt ggattgcagg 2100
catgagccac tgcacccagc cctgtattct tattcttcag atatttattt ttcttttcac 2160
tgttttaaaa taaaaccaa gtattgataa aaaaaaa 2197

```

<210> 12

<211> 164

<212> PRT

<213> Homo sapiens

<400> 12

```

Met Trp Arg Cys Pro Leu Gly Leu Leu Leu Leu Leu Pro Leu Ala Gly
  1                      5                      10                      15

```

```

His Leu Ala Leu Gly Ala Gln Gln Gly Arg Gly Arg Arg Glu Leu Ala
      20                      25                      30

```

```

Pro Gly Leu His Leu Arg Gly Ile Arg Asp Ala Gly Gly Arg Tyr Cys
      35                      40                      45

```

```

Gln Glu Gln Asp Leu Cys Cys Arg Gly Arg Ala Asp Asp Cys Ala Leu
      50                      55                      60

```

```

Pro Tyr Leu Gly Ala Ile Cys Tyr Cys Asp Leu Phe Cys Asn Arg Thr
      65                      70                      75                      80

```

```

Val Ser Asp Cys Cys Pro Asp Phe Trp Asp Phe Cys Leu Gly Val Pro
      85                      90                      95

```

```

Pro Pro Phe Pro Pro Ile Gln Gly Cys Met His Gly Gly Arg Ile Tyr
      100                      105                      110

```

```

Pro Val Leu Gly Thr Tyr Trp Asp Asn Cys Asn Arg Cys Thr Cys Gln
      115                      120                      125

```

```

Glu Asn Arg Gln Trp His Gly Gly Ser Arg His Asp Gln Ser His Gln
      130                      135                      140

```

```

Pro Gly Gln Leu Trp Leu Ala Gly Trp Glu Pro Gln Arg Leu Leu Gly
      145                      150                      155                      160

```

His Asp Pro Gly

108120"02E60660

<210> 13  
 <211> 533  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (33)  
 <223> a, t, c or g

<220>  
 <221> modified\_base  
 <222> (80)  
 <223> a, t, c or g

<220>  
 <221> modified\_base  
 <222> (94)  
 <223> a, t, c or g

<220>  
 <221> modified\_base  
 <222> (144)  
 <223> a, t, c or g

<220>  
 <221> modified\_base  
 <222> (188)  
 <223> a, t, c or g

<400> 13  
 aggctccttg gccctttttc cacagcaagc ttntgcnatc ccgattcggt gtetcaaatac 60  
 caattctctt gggacacatn acgcctgtcc tttngcccca gaacctgctg tcttgtacac 120  
 ccaccagcag cagggctgcc gcgntgggag tctcgatggt gcctgggtgg tcttgcgtcg 180  
 ccgagggntg gtgtctgacc actgctaccc cttctcgggc cgtgaacgag acgaggctgg 240  
 ccctgcgccc ccctgtatga tgcacagccg agccatgggt cgggggcaagc gccaggccac 300  
 tgcccactgc cccaacagct atgttaataa caatgacatc taccaggtca ctctgtcta 360  
 ccgcctcggc tccaacgaca aggagatcat gaaggagctg atggagaatg gccctgtcca 420  
 agccctcatg gaggtgcatg aggacttctt cctatacaag ggagggcatc acagccacac 480  
 gccagtgagc cttgggaggc cagagagata ccgccggcat gggacccact cag 533

<210> 14  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 14

24

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

22

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

50

<213> Homo sapiens

gctgcttgcc	ctgttgatgg	caggcttggc	cctgcagcca	ggcactgcc	tgctgtgcta	60
ctcctgcaaa	gcccagggtga	gcaacgagga	ctgcctgcag	gtggagaact	gcacccagct	120
gggggagcag	tgctggaccg	cgcgcacccg	cgcagttggc	ctcctgaccg	tcatcagcaa	180
aggctgcagc	ttgaactgcg	tggatgactc	acaggactac	tacgtgggca	agaagaacat	240
cacgtgctgt	gacaccgact	tgtgcaacgc	cagcggggcc	catgccctgc	agccggctgc	300
cgccatcctt	gcgctgctcc	ctgcactcgg	cctgctgctc	tggggacccg	gccagctata	360
ggctctgggg	ggccccgctg	cagcccacac	tgggtgtggt	gccccaggcc	tctgtgccac	420
tcctcacaga	cctggcccag	tgggagcctg	tcttgggtcc	tgaggcacat	cctaacgcaa	480
gtctgaccat	gtatgtctgc	acccctgtcc	cccaccctga	ccctcccattg	gccctctcca	540
ggactcccac	ccggcagatc	agctctagt	acacagatcc	gcctgcagat	ggccccctcca	600
accctctctg	ctgctgtttc	catggcccag	cattctccac	ccttaacct	gtgctcaggc	660
acctcttccc	ccagggaagc	tcccctggcc	accccattca	tgacttgagc	caggtctggg	720
ccgtgggtgc	cccgcagccc	atcaggggac	aggcactcag	gagggcccag	taaaggctga	780
gatgaagtgg	actgagttag	actggaggac	aagagtcgac	gtgagttcct	gggagctccc	840
agagatgggg	cctggaggcc	tggagggaag	ggccaggcct	cacattcctg	gggctccctg	900
aatggcagcc	tgagcacagc	gtaggccctt	aataaacacc	tgttggataa	qccaaaaaaaa	960

<213> Homo sapiens

&lt;400&gt; 18

Met Thr His Arg Thr Thr Thr Trp Ala Arg Arg Thr Ser Arg Ala Val  
 1 5 10 15

Thr Pro Thr Cys Ala Thr Pro Ala Gly Pro Met Pro Cys Ser Arg Leu  
 20 25 30

Pro Pro Ser Leu Arg Cys Ser Leu His Ser Ala Cys Cys Ser Gly Asp  
 35 40 45

Pro Ala Ser Tyr Arg Leu Trp Gly Ala Pro Leu Gln Pro Thr Leu Gly  
 50 55 60

Val Val Pro Gln Ala Ser Val Pro Leu Leu Thr Asp Leu Ala Gln Trp  
 65 70 75 80

Glu Pro Val Leu Val Pro Glu Ala His Pro Asn Ala Ser Leu Thr Met  
 85 90 95

Tyr Val Cys Thr Pro Val Pro His Pro Asp Pro Pro Met Ala Leu Ser  
 100 105 110

Arg Thr Pro Thr Arg Gln Ile Ser Ser Ser Asp Thr Asp Pro Pro Ala  
 115 120 125

Asp Gly Pro Ser Asn Pro Leu Cys Cys Cys Phe His Gly Pro Ala Phe  
 130 135 140

Ser Thr Leu Asn Pro Val Leu Arg His Leu Phe Pro Gln Glu Ala Phe  
 145 150 155 160

Pro Ala His Pro Ile Tyr Asp Leu Ser Gln Val Trp Ser Val Val Ser  
 165 170 175

Pro Ala Pro Ser Arg Gly Gln Ala Leu Arg Arg Ala Gln  
 180 185

&lt;210&gt; 19

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 19

tgctgtgcta ctctgcaaa gccc

24

&lt;210&gt; 20

&lt;211&gt; 24

&lt;212&gt; DNA

T03T20"02E6060



&lt;400&gt; 23

Met Gly Ala Ala Arg Leu Leu Pro Asn Leu Thr Leu Cys Leu Gln Leu  
 1 5 10 15

Leu Ile Leu Cys Cys Gln Thr Gln Tyr Val Arg Asp Gln Gly Ala Met  
 20 25 30

Thr Asp Gln Leu Ser Arg Arg Gln Ile Arg Glu Tyr Gln Leu Tyr Ser  
 35 40 45

Arg Thr Ser Gly Lys His Val Gln Val Thr Gly Arg Arg Ile Ser Ala  
 50 55 60

Thr Ala Glu Asp Gly Asn Lys Phe Ala Lys Leu Ile Val Glu Thr Asp  
 65 70 75 80

Thr Phe Gly Ser Arg Val Arg Ile Lys Gly Ala Glu Ser Glu Lys Tyr  
 85 90 95

Ile Cys Met Asn Lys Arg Gly Lys Leu Ile Gly Lys Pro Ser Gly Lys  
 100 105 110

Ser Lys Asp Cys Val Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr  
 115 120 125

Ala Phe Gln Asn Ala Arg His Glu Gly Trp Phe Met Ala Phe Thr Arg  
 130 135 140

Gln Gly Arg Pro Arg Gln Ala Ser Arg Ser Arg Gln Asn Gln Arg Glu  
 145 150 155 160

Ala His Phe Ile Lys Arg Leu Tyr Gln Gly Gln Leu Pro Phe Pro Asn  
 165 170 175

His Ala Glu Lys Gln Lys Gln Phe Glu Phe Val Gly Ser Ala Pro Thr  
 180 185 190

Arg Arg Thr Lys Arg Thr Arg Arg Pro Gln Pro Leu Thr  
 195 200 205

&lt;210&gt; 24

&lt;211&gt; 28

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 24

cagtacgtga gggaccaggg cgccatga

28

&lt;210&gt; 25

T08120"02E60660

<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 25  
 ccggtgacct gcacgtgctt gccca 24

<210> 26  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<220>  
 <221> modified\_base  
 <222> (21)  
 <223> a, t, c or g

<400> 26  
 gcggatctgc cgctgctca nctggctcgg catggcgccc t 41

<210> 27  
 <211> 2479  
 <212> DNA  
 <213> Homo sapiens

<400> 27  
 acttgccatc acctgttgcc agtgtggaaa aattctccct gttgaatttt ttgcacatgg 60  
 aggacagcag caaagagggc aacacaggct gataagacca gagacagcag ggagattatt 120  
 ttaccatacg ccctcaggac gtccctctta gctggagttc tggacttcaa cagaacccca 180  
 tccagtcatt ttgattttgc tgtttatatt ttttttcttt ttctttttcc caccacattg 240  
 tatttttatt ccgtacttca gaaatgggac tacagaccac aaagtggccc agccatgggg 300  
 cttttttcct gaagtcttgg cttatcattt ccctggggct ctactcacag gtgtccaaac 360  
 tcctggcctg ccctagtgtg tgcgcgtgcg acaggaactt tgtctactgt aatgagcgaa 420  
 gcttgacctc agtgccctct gggatcccgg agggcgtaac cgtactctac ctccacaaca 480  
 accaaattaa taatgctgga tttcctgcag aactgcacaa tgtacagtcg gtgcacacgg 540  
 tctacctgta tggcaacca ctggacgaat tccccatgaa ccttcccaag aatgtcagag 600  
 ttctccattt gcaggaaaac aatattcaga ccatttcacg ggctgctctt gccagctct 660  
 tgaagcttga agagctgcac ctggatgaca actccatata cacagtgggg gtggaagacg 720  
 gggccttcct ggaggtatt agcctcaa atgtgttttt gtctaagaat cacctgagca 780  
 gtgtgcctgt tgggcttctt gtggacttgc aagagctgag agtggatgaa aatcgaattg 840  
 ctgtcatata cgacatggcc ttccagaatc tcacgagctt ggagcgtctt attgtggacg 900  
 ggaacctcct gaccaacaag ggtatcgccg agggcacctt cagccatctc accaagctca 960  
 aggaattttc aattgtacgt aattcgctgt cccaccctcc tcccgatctc ccaggtagcg 1020  
 atctgatcag gctctatttg caggacaacc agataaacca cattcctttg acagccttct 1080  
 caaatctgcg taagctggaa cggctggata tatccaacaa ccaactgcgg atgctgactc 1140

aagggggtttt tgataatctc tccaacctga agcagctcac tgctcggaat aacccttggt 1200  
tttgtgactg cagtattaaa tgggtcacag aatgggtcaa atatatccct tcattctctca 1260  
acgtgcgggg tttcatgtgc caaggtcctg aacaagtccg ggggatggcc gtcaggggaat 1320  
taaataatgaa tcttttgtcc tgtcccacca cgaccccccg cctgcctctc ttcaccccag 1380  
ccccaagtac agcttctccg accactcagc ctcccaccct ctctattcca aaccctagca 1440  
gaagctacac gcctccaact cctaccacat cgaaacttcc cacgattcct gactgggatg 1500  
gcagagaaaag agtgacccca cctatttctg aacggatcca gctctctatc cattttgtga 1560  
atgatacttc cattcaagtc agctggctct ctctcttcac cgtgatggca taaaaactca 1620  
catgggtgaa aatgggccac agtttagtag ggggcatcgt tcaggagcgc atagtcagcg 1680  
gtgagaagca acacctgagc ctggttaact tagagccccg atccacctat cggatttgtt 1740  
tagtgccact ggatgctttt aactaccgcg cggtagaaga caccatttgt tcagaggcca 1800  
ccacccatgc ctctatctg aacaacggca gcaacacagc gtccagccat gagcagacga 1860  
cgtcccacag catgggctcc ccctttctgc tggcgggctt gatcgggggc cgggtgatat 1920  
ttgtgctggt ggtcttgctc agcgtctttt gctggcatat gcacaaaaag gggcgctaca 1980  
cctcccagaa gtggaaatac aaccggggcc ggcggaaga tgattattgc gaggcaggca 2040  
ccaagaagga caactccatc ctggagatga cagaaaccag ttttcagatc gtctccttaa 2100  
ataacgatca actccttaaa ggagatttca gactgcagcc catttacacc ccaaatgggg 2160  
gcattaatta cacagactgc catatcccca acaacatgcg atactgcaac agcagcgtgc 2220  
cagacctgga gcaactgcat acgtgacagc cagaggccca gcgttatcaa ggcggacaat 2280  
tagactcttg agaacacact cgtgtgtgca cataaagaca cgcagattac atttgataaa 2340  
tggtacacag atgcatttgt gcatttgaat actctgtaat ttatacggtg tactatataa 2400  
tgggatttaa aaaaagtgtc atcttttcta tttcaagtta attacaaaca gttttgtaac 2460  
tctttgcttt ttaaatctt 2479

<210> 28

<211> 660

<212> PRT

<213> Homo sapiens

<400> 28

Met Gly Leu Gln Thr Thr Lys Trp Pro Ser His Gly Ala Phe Phe Leu  
1 5 10 15  
Lys Ser Trp Leu Ile Ile Ser Leu Gly Leu Tyr Ser Gln Val Ser Lys  
20 25 30  
Leu Leu Ala Cys Pro Ser Val Cys Arg Cys Asp Arg Asn Phe Val Tyr  
35 40 45  
Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly Ile Pro Glu Gly  
50 55 60  
Val Thr Val Leu Tyr Leu His Asn Asn Gln Ile Asn Asn Ala Gly Phe  
65 70 75 80  
Pro Ala Glu Leu His Asn Val Gln Ser Val His Thr Val Tyr Leu Tyr  
85 90 95  
Gly Asn Gln Leu Asp Glu Phe Pro Met Asn Leu Pro Lys Asn Val Arg  
100 105 110  
Val Leu His Leu Gln Glu Asn Asn Ile Gln Thr Ile Ser Arg Ala Ala  
115 120 125

0909320-071301



Leu	Ala	Gln	Leu	Leu	Lys	Leu	Glu	Glu	Leu	His	Leu	Asp	Asp	Asn	Ser
130						135				140					
Ile	Ser	Thr	Val	Gly	Val	Glu	Asp	Gly	Ala	Phe	Arg	Glu	Ala	Ile	Ser
145				150						155				160	
Leu	Lys	Leu	Leu	Phe	Leu	Ser	Lys	Asn	His	Leu	Ser	Ser	Val	Pro	Val
				165				170						175	
Gly	Leu	Pro	Val	Asp	Leu	Gln	Glu	Leu	Arg	Val	Asp	Glu	Asn	Arg	Ile
		180						185				190			
Ala	Val	Ile	Ser	Asp	Met	Ala	Phe	Gln	Asn	Leu	Thr	Ser	Leu	Glu	Arg
		195				200						205			
Leu	Ile	Val	Asp	Gly	Asn	Leu	Leu	Thr	Asn	Lys	Gly	Ile	Ala	Glu	Gly
210						215				220					
Thr	Phe	Ser	His	Leu	Thr	Lys	Leu	Lys	Glu	Phe	Ser	Ile	Val	Arg	Asn
225				230						235				240	
Ser	Leu	Ser	His	Pro	Pro	Pro	Asp	Leu	Pro	Gly	Thr	His	Leu	Ile	Arg
				245				250						255	
Leu	Tyr	Leu	Gln	Asp	Asn	Gln	Ile	Asn	His	Ile	Pro	Leu	Thr	Ala	Phe
		260						265				270			
Ser	Asn	Leu	Arg	Lys	Leu	Glu	Arg	Leu	Asp	Ile	Ser	Asn	Asn	Gln	Leu
275						280						285			
Arg	Met	Leu	Thr	Gln	Gly	Val	Phe	Asp	Asn	Leu	Ser	Asn	Leu	Lys	Gln
290						295				300					
Leu	Thr	Ala	Arg	Asn	Asn	Pro	Trp	Phe	Cys	Asp	Cys	Ser	Ile	Lys	Trp
305				310						315				320	
Val	Thr	Glu	Trp	Leu	Lys	Tyr	Ile	Pro	Ser	Ser	Leu	Asn	Val	Arg	Gly
				325				330						335	
Phe	Met	Cys	Gln	Gly	Pro	Glu	Gln	Val	Arg	Gly	Met	Ala	Val	Arg	Glu
		340						345				350			
Leu	Asn	Met	Asn	Leu	Leu	Ser	Cys	Pro	Thr	Thr	Thr	Pro	Gly	Leu	Pro
355						360						365			
Leu	Phe	Thr	Pro	Ala	Pro	Ser	Thr	Ala	Ser	Pro	Thr	Thr	Gln	Pro	Pro
370						375				380					
Thr	Leu	Ser	Ile	Pro	Asn	Pro	Ser	Arg	Ser	Tyr	Thr	Pro	Pro	Thr	Pro
385				390						395				400	
Thr	Thr	Ser	Lys	Leu	Pro	Thr	Ile	Pro	Asp	Trp	Asp	Gly	Arg	Glu	Arg

				405					410					415			
Val	Thr	Pro	Pro	Ile	Ser	Glu	Arg	Ile	Gln	Leu	Ser	Ile	His	Phe	Val		
			420					425					430				
Asn	Asp	Thr	Ser	Ile	Gln	Val	Ser	Trp	Leu	Ser	Leu	Phe	Thr	Val	Met		
		435					440					445					
Ala	Tyr	Lys	Leu	Thr	Trp	Val	Lys	Met	Gly	His	Ser	Leu	Val	Gly	Gly		
	450					455					460						
Ile	Val	Gln	Glu	Arg	Ile	Val	Ser	Gly	Glu	Lys	Gln	His	Leu	Ser	Leu		
465					470				475						480		
Val	Asn	Leu	Glu	Pro	Arg	Ser	Thr	Tyr	Arg	Ile	Cys	Leu	Val	Pro	Leu		
				485					490					495			
Asp	Ala	Phe	Asn	Tyr	Arg	Ala	Val	Glu	Asp	Thr	Ile	Cys	Ser	Glu	Ala		
			500					505					510				
Thr	Thr	His	Ala	Ser	Tyr	Leu	Asn	Asn	Gly	Ser	Asn	Thr	Ala	Ser	Ser		
		515					520					525					
His	Glu	Gln	Thr	Thr	Ser	His	Ser	Met	Gly	Ser	Pro	Phe	Leu	Leu	Ala		
	530					535					540						
Gly	Leu	Ile	Gly	Gly	Ala	Val	Ile	Phe	Val	Leu	Val	Val	Leu	Leu	Ser		
545					550				555						560		
Val	Phe	Cys	Trp	His	Met	His	Lys	Lys	Gly	Arg	Tyr	Thr	Ser	Gln	Lys		
				565					570					575			
Trp	Lys	Tyr	Asn	Arg	Gly	Arg	Arg	Lys	Asp	Asp	Tyr	Cys	Glu	Ala	Gly		
			580					585					590				
Thr	Lys	Lys	Asp	Asn	Ser	Ile	Leu	Glu	Met	Thr	Glu	Thr	Ser	Phe	Gln		
			595				600					605					
Ile	Val	Ser	Leu	Asn	Asn	Asp	Gln	Leu	Leu	Lys	Gly	Asp	Phe	Arg	Leu		
	610					615					620						
Gln	Pro	Ile	Tyr	Thr	Pro	Asn	Gly	Gly	Ile	Asn	Tyr	Thr	Asp	Cys	His		
625					630					635					640		
Ile	Pro	Asn	Asn	Met	Arg	Tyr	Cys	Asn	Ser	Ser	Val	Pro	Asp	Leu	Glu		
				645					650					655			
His	Cys	His	Thr														
			660														

<210> 29  
 <211> 21  
 <212> DNA

0909330.071801

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 29

cggtctacct gtatggcaac c

21

<210> 30

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 30

gcaggacaac cagataaacc ac

22

<210> 31

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 31

acgcagattt gagaaggctg tc

22

<210> 32

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 32

ttcacgggct gctcttgccc agctcttgaa gcttgaagag ctgcac

46

<210> 33

<211> 3449

<212> DNA

<213> Homo sapiens

<400> 33

acttgagca agcggcggcg gcggagacag aggcagaggc agaagctggg gctccgtcct 60  
cgctccac gagcgatccc cgaggagagc cgcggccctc ggcgaggcga agaggccgac 120

0909320-071801

gaggaagacc	cgggtggctg	cgccctgccc	tcgcttccca	ggcgccggcg	gctgcagcct	180
tgccctctt	gctcgcttg	aaaatggaaa	agatgctcgc	aggctgcttt	ctgctgatcc	240
tcggacagat	cgtcctctc	cctgccgagg	ccagggagcg	gtcacgtggg	aggtccatct	300
ctaggggcag	acacgctcgg	accacccgc	agacggccct	tctggagagt	tcctgtgaga	360
acaagcgggc	agacctgggt	ttcatcattg	acagctctcg	cagtgtcaac	acccatgact	420
atgcaaaggt	caaggagttc	atcgtggaca	tcttgcaatt	cttggacatt	ggtcctgatg	480
tcacccgagt	gggcctgctc	caatatggca	gcactgtcaa	gaatgagttc	tcctcaaga	540
ccttcaagag	gaagtccgag	gtggagcgtg	ctgtcaagag	gatgcggcat	ctgtccacgg	600
gcaccatgac	tgggctggcc	atccagtatg	ccctgaacat	cgattctca	gaagcagagg	660
gggcccggcc	cctgagggag	aatgtgccac	gggtcataat	gatcgtgaca	gatgggagac	720
ctcaggactc	cgtggccgag	gtggctgcta	aggcacggga	cacgggcata	ctaactcttg	780
ccattgggtg	gggccaggta	gacttcaaca	ccttgaagtc	cattgggagt	gagcccatg	840
aggaccatgt	cttccttggt	gccaatttca	gccagattga	gacgctgacc	tcctgtttcc	900
agaagaagtt	gtgcacggcc	cacatgtgca	gcaccctgga	gcataactgt	gcccacttct	960
gcataacat	ccctgggtca	tacgtctgca	ggtgcaaaaca	aggctacatt	ctcaactcgg	1020
atcagacgac	ttgcagaatc	caggatctgt	gtgccatgga	ggaccacaac	tgtgagcagc	1080
tctgtgtgaa	tgtgccgggc	tccttcgtct	gccagtgtca	cagtggctac	gccctggctg	1140
aggatgggaa	gaggtgtgtg	gctgtggact	actgtgcctc	agaaaaccac	ggatgtgaac	1200
atgagtgtgt	aaatgctgat	ggctcctacc	tttgccagtg	ccatgaagga	tttgccttta	1260
accagatga	aaaaacgtgc	acaaggatca	actactgtgc	actgaacaaa	ccgggctgtg	1320
agcatgagtg	cgtcaacatg	gaggagagct	actactgccg	ctgccaccgt	ggctacactc	1380
tggaccccaa	tggcaaaaacc	tgcagccgag	tggaccactg	tgcacagcag	gaccatggct	1440
gtgagcagct	gtgtctgaac	acggaggatt	ccttcgtctg	ccagtgtctca	gaaggcttcc	1500
tcataacga	ggacctcaag	acctgctccc	gggtggatta	ctgcctgctg	agtgaccatg	1560
gttgtgaata	ctcctgtgtc	aacatggaca	gatcctttgc	ctgtcagtg	cctgagggac	1620
acgtgctccg	cagcgatggg	aagacgtgtg	caaaattgga	ctcttgtgct	ctgggggacc	1680
acggttgtga	acattcgtgt	gtaagcagtg	aagattcgtt	tgtgtgccag	tgtttgaag	1740
gttatatact	ccgtgaagat	ggaaaaacct	gcagaaggaa	agatgtctgc	caagctatag	1800
accatggctg	tgaacacatt	tgtgtgaaca	gtgacgactc	atacacgtgc	gagtgtttgg	1860
agggattccg	gctcgctgag	gatgggaaac	gctgccgaag	gaaggatgtc	tgcaaatcaa	1920
cccaccatgg	ctgcgaacac	atttgtgtta	ataatgggaa	ttctacatc	tgcaaatgct	1980
cagagggatt	tgttctagct	gaggacggaa	gacggtgcaa	gaaatgcact	gaaggcccaa	2040
ttgacctgg	ctttgtgatc	gatggatcca	agagctcttg	agaagagaat	tttgaggctg	2100
tgaagcagtt	tgtcactgga	attatagatt	ccttgacaat	ttccccaaa	gccgtctgag	2160
tggggctgct	ccagtattcc	acacaggtcc	acacagagtt	cactctgaga	aacttcaact	2220
cagccaaaga	catgaaaaaa	gccgtggccc	acatgaaata	catgggaaag	ggctctatga	2280
ctgggctggc	cctgaaacac	atgtttgaga	gaagttttac	ccaaggagaa	ggggccaggc	2340
ccctttccac	aagggtgccc	agagcagcca	ttgtgttcac	cgacggacgg	gctcaggatg	2400
acgtctccga	gtgggccag	aaagccaagg	ccaatggtat	cactatgtat	gctgttgggg	2460
taggaaaagc	cattgaggag	gaactacaag	agattgcctc	tgagcccaca	aacaagcatc	2520
tcttctatgc	cgaagacttc	agcacaatgg	atgagataag	tgaaaaactc	aagaaaggca	2580
tctgtgaagc	tctagaagac	tccgatggaa	gacaggactc	tccagcaggg	gaactgcca	2640
aaacggtcca	acagccaaca	gaatctgagc	cagtcacccat	aaatatccaa	gacctacttt	2700
cctgttctaa	ttttgcagtg	caacacagat	atctgtttga	agaagacaat	cttttacggt	2760
ctacacaaaa	gctttcccat	tcaacaaaac	cttcagggaag	ccctttggaa	gaaaaacacg	2820
atcaatgcaa	atgtgaaaac	cttataatgt	tccagaacct	tgcaaacgaa	gaagtaagaa	2880
aattaacaca	gcgcttagaa	gaaatgacac	agagaatgga	agccctggaa	aatcgctga	2940
gatacagatg	aagattagaa	atcgcgacac	atgtgtagtc	attgtatcac	ggattacaat	3000
gaacgcagtg	cagagcccca	aagctcaggc	tattgttaaa	tcaataatgt	tgtgaagtaa	3060
aacaatcagt	actgagaaac	ctggtttgcc	acagaacaaa	gacaagaagt	atacactaac	3120
ttgtataaat	ttatctagga	aaaaaatcct	tcagaattct	aagatgaatt	taccaggtga	3180
gaatgaataa	gctatgcaag	gtattttgta	atatactgtg	gacacaactt	gcttctgcct	3240
catcctgcct	tagtgtgcaa	tctcatttga	ctatacgata	aagtttgcac	agtcttactt	3300

ctgtagaaca ctggccatag gaaatgctgt tttttgtac tggactttac cttgatatat 3360  
 gtatatggat gtatgcataa aatcatagga catatgtact tgtggaacaa gttggatttt 3420  
 ttatacaata ttaaaattca ccacttcag 3449

<210> 34

<211> 915

<212> PRT

<213> Homo sapiens

<400> 34

Met	Glu	Lys	Met	Leu	Ala	Gly	Cys	Phe	Leu	Leu	Ile	Leu	Gly	Gln	Ile	
1				5					10					15		
Val	Leu	Leu	Pro	Ala	Glu	Ala	Arg	Glu	Arg	Ser	Arg	Gly	Arg	Ser	Ile	
			20					25					30			
Ser	Arg	Gly	Arg	His	Ala	Arg	Thr	His	Pro	Gln	Thr	Ala	Leu	Leu	Glu	
		35					40					45				
Ser	Ser	Cys	Glu	Asn	Lys	Arg	Ala	Asp	Leu	Val	Phe	Ile	Ile	Asp	Ser	
	50					55					60					
Ser	Arg	Ser	Val	Asn	Thr	His	Asp	Tyr	Ala	Lys	Val	Lys	Glu	Phe	Ile	
65					70					75					80	
Val	Asp	Ile	Leu	Gln	Phe	Leu	Asp	Ile	Gly	Pro	Asp	Val	Thr	Arg	Val	
				85					90					95		
Gly	Leu	Leu	Gln	Tyr	Gly	Ser	Thr	Val	Lys	Asn	Glu	Phe	Ser	Leu	Lys	
			100					105					110			
Thr	Phe	Lys	Arg	Lys	Ser	Glu	Val	Glu	Arg	Ala	Val	Lys	Arg	Met	Arg	
		115					120						125			
His	Leu	Ser	Thr	Gly	Thr	Met	Thr	Gly	Leu	Ala	Ile	Gln	Tyr	Ala	Leu	
		130				135					140					
Asn	Ile	Ala	Phe	Ser	Glu	Ala	Glu	Gly	Ala	Arg	Pro	Leu	Arg	Glu	Asn	
145					150					155					160	
Val	Pro	Arg	Val	Ile	Met	Ile	Val	Thr	Asp	Gly	Arg	Pro	Gln	Asp	Ser	
				165					170					175		
Val	Ala	Glu	Val	Ala	Ala	Lys	Ala	Arg	Asp	Thr	Gly	Ile	Leu	Ile	Phe	
			180					185					190			
Ala	Ile	Gly	Val	Gly	Gln	Val	Asp	Phe	Asn	Thr	Leu	Lys	Ser	Ile	Gly	
		195					200					205				
Ser	Glu	Pro	His	Glu	Asp	His	Val	Phe	Leu	Val	Ala	Asn	Phe	Ser	Gln	
	210					215					220					
Ile	Glu	Thr	Leu	Thr	Ser	Val	Phe	Gln	Lys	Lys	Leu	Cys	Thr	Ala	His	

09909320-071801

225		230		235		240
Met Cys Ser Thr	Leu Glu His Asn Cys	Ala His Phe Cys	Ile Asn Ile			
	245	250	255			
Pro Gly Ser Tyr	Val Cys Arg Cys	Lys Gln Gly Tyr	Ile Leu Asn Ser			
	260	265	270			
Asp Gln Thr Thr	Cys Arg Ile Gln	Asp Leu Cys Ala	Met Glu Asp His			
	275	280	285			
Asn Cys Glu Gln	Leu Cys Val Asn	Val Pro Gly Ser	Phe Val Cys Gln			
	290	295	300			
Cys Tyr Ser Gly	Tyr Ala Leu Ala	Glu Asp Gly Lys	Arg Cys Val Ala			
	305	310	315			320
Val Asp Tyr Cys	Ala Ser Glu Asn	His Gly Cys Glu	His Glu Cys Val			
	325	330	335			
Asn Ala Asp Gly	Ser Tyr Leu Cys	Gln Cys His Glu	Gly Phe Ala Leu			
	340	345	350			
Asn Pro Asp Glu	Lys Thr Cys Thr	Arg Ile Asn Tyr	Cys Ala Leu Asn			
	355	360	365			
Lys Pro Gly Cys	Glu His Glu Cys	Val Asn Met Glu	Glu Ser Tyr Tyr			
	370	375	380			
Cys Arg Cys His	Arg Gly Tyr Thr	Leu Asp Pro Asn	Gly Lys Thr Cys			
	385	390	395			400
Ser Arg Val Asp	His Cys Ala Gln	Gln Asp His Gly	Cys Glu Gln Leu			
	405	410	415			
Cys Leu Asn Thr	Glu Asp Ser Phe	Val Cys Gln Cys	Ser Glu Gly Phe			
	420	425	430			
Leu Ile Asn Glu	Asp Leu Lys Thr	Cys Ser Arg Val	Asp Tyr Cys Leu			
	435	440	445			
Leu Ser Asp His	Gly Cys Glu Tyr	Ser Cys Val Asn	Met Asp Arg Ser			
	450	455	460			
Phe Ala Cys Gln	Cys Pro Glu Gly	His Val Leu Arg	Ser Asp Gly Lys			
	465	470	475			480
Thr Cys Ala Lys	Leu Asp Ser Cys	Ala Leu Gly Asp	His Gly Cys Glu			
	485	490	495			
His Ser Cys Val	Ser Ser Glu Asp	Ser Phe Val Cys	Gln Cys Phe Glu			
	500	505	510			

T03F70-02E60660

Gly Tyr Ile Leu Arg Glu Asp Gly Lys Thr Cys Arg Arg Lys Asp Val  
 515 520 525  
 Cys Gln Ala Ile Asp His Gly Cys Glu His Ile Cys Val Asn Ser Asp  
 530 535 540  
 Asp Ser Tyr Thr Cys Glu Cys Leu Glu Gly Phe Arg Leu Ala Glu Asp  
 545 550 555 560  
 Gly Lys Arg Cys Arg Arg Lys Asp Val Cys Lys Ser Thr His His Gly  
 565 570 575  
 Cys Glu His Ile Cys Val Asn Asn Gly Asn Ser Tyr Ile Cys Lys Cys  
 580 585 590  
 Ser Glu Gly Phe Val Leu Ala Glu Asp Gly Arg Arg Cys Lys Lys Cys  
 595 600 605  
 Thr Glu Gly Pro Ile Asp Leu Val Phe Val Ile Asp Gly Ser Lys Ser  
 610 615 620  
 Leu Gly Glu Glu Asn Phe Glu Val Val Lys Gln Phe Val Thr Gly Ile  
 625 630 635 640  
 Ile Asp Ser Leu Thr Ile Ser Pro Lys Ala Ala Arg Val Gly Leu Leu  
 645 650 655  
 Gln Tyr Ser Thr Gln Val His Thr Glu Phe Thr Leu Arg Asn Phe Asn  
 660 665 670  
 Ser Ala Lys Asp Met Lys Lys Ala Val Ala His Met Lys Tyr Met Gly  
 675 680 685  
 Lys Gly Ser Met Thr Gly Leu Ala Leu Lys His Met Phe Glu Arg Ser  
 690 695 700  
 Phe Thr Gln Gly Glu Gly Ala Arg Pro Leu Ser Thr Arg Val Pro Arg  
 705 710 715 720  
 Ala Ala Ile Val Phe Thr Asp Gly Arg Ala Gln Asp Asp Val Ser Glu  
 725 730 735  
 Trp Ala Ser Lys Ala Lys Ala Asn Gly Ile Thr Met Tyr Ala Val Gly  
 740 745 750  
 Val Gly Lys Ala Ile Glu Glu Glu Leu Gln Glu Ile Ala Ser Glu Pro  
 755 760 765  
 Thr Asn Lys His Leu Phe Tyr Ala Glu Asp Phe Ser Thr Met Asp Glu  
 770 775 780  
 Ile Ser Glu Lys Leu Lys Lys Gly Ile Cys Glu Ala Leu Glu Asp Ser  
 785 790 795 800

05909320-071804

Asp Gly Arg Gln Asp Ser Pro Ala Gly Glu Leu Pro Lys Thr Val Gln  
805 810 815

Gln Pro Thr Glu Ser Glu Pro Val Thr Ile Asn Ile Gln Asp Leu Leu  
820 825 830

Ser Cys Ser Asn Phe Ala Val Gln His Arg Tyr Leu Phe Glu Glu Asp  
835 840 845

Asn Leu Leu Arg Ser Thr Gln Lys Leu Ser His Ser Thr Lys Pro Ser  
850 855 860

Gly Ser Pro Leu Glu Glu Lys His Asp Gln Cys Lys Cys Glu Asn Leu  
865 870 875 880

Ile Met Phe Gln Asn Leu Ala Asn Glu Glu Val Arg Lys Leu Thr Gln  
885 890 895

Arg Leu Glu Glu Met Thr Gln Arg Met Glu Ala Leu Glu Asn Arg Leu  
900 905 910

Arg Tyr Arg  
915

<210> 35

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 35

gtgaccctgg ttgtgaatac tcc

23

<210> 36

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 36

acagccatgg tctatagctt gg

22

<210> 37

<211> 45

<212> DNA

<213> Artificial Sequence

09009320.071801



<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

gcctgtcagt qtcctgaagg acacgtgctc cgcagcgaag ggaag

45

<211> 1813

<213> Homo sapiens

ggagccgccc	tgggtgtcag	cggctcggct	ccgcgcacg	ctcgggccgt	cgcgcagcct	60
cggcacctgc	aggtccgtgc	gtcccgcggc	tggcgcocct	gactccgtcc	cggccagggg	120
gggccatgat	ttccctcccg	gggcccctgg	tgaccaactt	gctgcggttt	ttgttccttg	180
ggctgagtgc	cctcgcgcc	ccctcgcggg	cccagctgca	actgcacttg	ccgcccaacc	240
ggttgcaggc	ggtggaggga	ggggaagtgg	tgttccagc	gtggtacacc	ttgcacgggg	300
aggtgtcttc	atcccagcca	tgggaggtgc	ccttttgtgat	gtggttcttc	aaacagaaag	360
aaaaggagga	tcaggtgttg	tcctacatca	atggggtcac	aacaagcaaa	cctggagtat	420
ccttggtcta	ctccatgccc	tcccggaacc	tgtccctgcg	gctggagggt	ctccaggaga	480
aagactctgg	cccctacagc	tgctccgtga	atgtgcaaga	caaacaaggc	aaatctaggg	540
gccacagcat	caaaacctta	gaactcaatg	tactggttcc	tccagctcct	ccatcctgcc	600
gtctccaggg	tgtgccccat	gtgggggcaa	acgtgacctt	gagctgccag	tctccaagga	660
gtaagcccg	tgtccaatac	cagtgggatc	ggcagcttcc	atccttccag	actttctttg	720
caccagcatt	agatgtcatc	cgtgggtctt	taagcctcac	caacctttcg	tcttccatgg	780
ctggagtcta	tgtctgcaag	gcccacaatg	aggtgggcac	tgcccaatgt	aatgtgacgc	840
tggaagtgag	cacaggccct	ggagctgcag	tggttgctgg	agctgttgtg	ggtacctctg	900
ttggactggg	gttgctggct	gggctggctc	tcttgtacca	ccgcgggggc	aaggccctgg	960
aggagccagc	caatgatatc	aaggaggatg	ccattgctcc	ccggaccttg	ccctggccca	1020
agagctcaga	cacaatctcc	aagaatggga	ccctttctct	tgtcacctcc	gcacgagccc	1080
tccggccacc	ccatggccct	cccaggcctg	gtgcattgac	ccccacgcc	agtctctcca	1140
gccaggccct	gccctcacca	agactgccc	cgacagatgg	ggcccacctt	caaccaatat	1200
cccccatccc	tgggtggggtt	tcttctctctg	gcttgagccg	catgggtgct	gtgcttgtga	1260
tgggtgctgc	ccagagtcaa	gctggctctc	tggatatgatg	acccaccac	tcattggcta	1320
aaggatttg	ggtctctcct	tcctataagg	gtcacctcta	gcacagaggc	ctgagtcatg	1380
ggaaagagtc	acactcctga	cccttagtac	tctgccccca	cctctcttta	ctgtgggaaa	1440
accatctcag	taagacctaa	gtgtccagga	gacagaagga	gaagaggaag	tggatctgga	1500
attgggagga	gcctccaccc	acccctgact	cctccttatg	aagccagctg	ctgaaattag	1560
ctactacca	agagtgagg	gcagagactt	ccagtcactg	agtctcccag	gcccccttga	1620
tctgtacccc	accctatct	aacaccaccc	ttggctccca	ctccagctcc	ctgtattgat	1680
ataacctgtc	aggctggctt	ggttaggttt	tactggggca	gaggataggg	aatctcttat	1740
taaaactaac	atgaaatatg	tgttgttttc	atttgcaaat	ttaaataaag	atacataatg	1800
tttgtatgaa	aaa					1813

<211> 390

<213> Homo sapiens

Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu

1	5	10	15
Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser Arg Ala Gln Leu Gln	20	25	30
Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly Gly Glu Val	35	40	45
Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln	50	55	60
Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys	65	70	75
Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro	85	90	95
Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn Leu Ser Leu Arg	100	105	110
Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr Ser Cys Ser Val	115	120	125
Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His Ser Ile Lys Thr	130	135	140
Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro Pro Ser Cys Arg Leu	145	150	155
Gln Gly Val Pro His Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser	165	170	175
Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro	180	185	190
Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser	195	200	205
Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys	210	215	220
Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu	225	230	235
Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val Gly	245	250	255
Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu Tyr His	260	265	270
Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile Lys Glu Asp	275	280	285

T08F20-02E60650

Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile  
290 295 300

Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Arg  
305 310 315 320

Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser  
325 330 335

Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly  
340 345 350

Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser  
355 360 365

Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser  
370 375 380

Gln Ala Gly Ser Leu Val  
385 390

<210> 40

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 40

agggtctcca ggagaaagac tc

22

<210> 41

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 41

attgtgggcc ttgcagacat agac

24

<210> 42

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

FOR 20" 02E60660

<400> 42  
 ggccacagca tcaaaacctt agaactcaat gtactggttc ctccagctcc 50  
  
 <210> 43  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 43  
 gtgtgacaca gcgtgggc 18  
  
 <210> 44  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 44  
 gaccggcagg cttctgcg 18  
  
 <210> 45  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 45  
 cagcagcttc agccaccagg agtgg 25  
  
 <210> 46  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 46  
 ctgagccgtg ggctgcagtc tcgc 24  
  
 <210> 47

0909320-01801  
 1081/0"02E60660

<211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 47  
 ccgactacga ctgggttcttc atcatgcagg atgacacata tgtgc 45

<210> 48  
 <211> 2822  
 <212> DNA  
 <213> Homo sapiens

<400> 48  
 cgccaccact ggcggccaccg ccaatgaaac gcctcccgcct cctagtgggtt ttttccactt 60  
 tgttgaattg ttccataact caaaattgca ccaagacacc ttgtctccca aatgcaaaat 120  
 gtgaaatacg caatggaatt gaagcctgct attgcaacat gggattttca ggaaatgggtg 180  
 tcacaatttg tgaagatgat aatgaatgtg gaaatttaac tcagtcctgt ggcgaaaatg 240  
 ctaattgcac taacacagaa ggaagttatt attgtatgtg tgtacctggc ttcagatcca 300  
 gcagtaacca agacagggtt atcactaatg atggaaccgt ctgtatagaa aatgtgaatg 360  
 caaactgcca tttagataat gtctgtatag ctgcaaatat taataaaact ttaacaaaaa 420  
 tcagatccat aaaagaacct gtggcttttg tacaagaagt ctatagaaat tctgtgacag 480  
 atctttcacc aacagatata attacatata tagaaatatt agctgaatca tcttcattac 540  
 taggttacaa gaacaacact atctcagcca aggacaccct ttctaactca actcttactg 600  
 aatttgtaaa aaccgtgaat aattttgttc aaagggatac atttgtagtt tgggacaagt 660  
 tatctgtgaa tcataggaga acacatctta caaaactcat gcacactgtt gaacaagcta 720  
 cttaaggat atcccagagc ttccaaaaga ccacagagtt tgatacaaat tcaacggata 780  
 tagctctcaa agttttcttt tttgattcat ataacatgaa acatattcat cctcatatga 840  
 atatggatgg agactacata aatatatttc caaagagaaa agctgcatat gattcaaatg 900  
 gcaatgttgc agttgcattt ttatattata agagtattgg tcctttgctt tcatcatctg 960  
 acaacttctt attgaaacct caaaattatg ataattctga agaggaggaa agagtcatat 1020  
 cttcagtaat ttcagtctca atgagctcaa acccaccac attatatgaa cttgaaaaaa 1080  
 taacatttac attaatgcat cgaaaggta cagataggta taggagtcta tgtgcatttt 1140  
 ggaattactc acctgatacc atgaatggca gctggtcttc agagggtgtg gagctgacat 1200  
 actcaaatga gaccacacc tcatgccgtc gtaatcacct gacacatttt gcaattttga 1260  
 tgtcctctgg tcttccatt ggtattaaag attataatat tcttacaagg atcactcaac 1320  
 taggaataat tatttcactg atttgtcttg ccatatgcat ttttaccttc tggttcttca 1380  
 gtgaaattca aagcaccagg acaacaattc acaaaaatct ttgctgtagc ctatttcttg 1440  
 ctgaacttgt ttttcttggt gggatcaata caaataactaa taagctcttc tgttcaatca 1500  
 ttgccggact gctacactac ttcttttttag ctgcttttgc atggatgtgc attgaaggca 1560  
 tacatctcta tctcattgtt gtgggtgtca tctacaacaa gggatttttg cacaagaatt 1620  
 tttatatctt tggctatcta agcccagccg tggtagttgg attttcggca gcactaggat 1680  
 acagatatta tggcacaacc aaagtatgtt ggcttagcac cgaaaacaac tttatttgga 1740  
 gttttatagg accagcatgc ctaatcattc ttgttaatct cttggctttt ggagtcacat 1800  
 tatacaaagt ttttcgtcac actgcagggt tgaaaccaga agttagttgc tttgagaaca 1860  
 taaggctctt tgcaagagga gccctcgctc ttctgttctt tctcggcacc acctggatct 1920  
 ttggggttct ccatgttgtg cacgcatcag tggttacagc ttacctcttc acagtcagca 1980  
 atgctttcca ggggatgttc atttttttat tctgtgtgt tttatctaga aagattcaag 2040  
 aagaatatta cagattgttc aaaaatgtcc cctgttgttt tggatgttta aggtaaacat 2100  
 agagaatggt ggataattac aactgcacaa aaataaaaat tccaagctgt ggatgaccaa 2160



	180		185		190
Glu Phe Val Lys Thr Val Asn Asn Phe Val Gln Arg Asp Thr Phe Val	195	200	205		
Val Trp Asp Lys Leu Ser Val Asn His Arg Arg Thr His Leu Thr Lys	210	215	220		
Leu Met His Thr Val Glu Gln Ala Thr Leu Arg Ile Ser Gln Ser Phe	225	230	235		240
Gln Lys Thr Thr Glu Phe Asp Thr Asn Ser Thr Asp Ile Ala Leu Lys	245	250	255		
Val Phe Phe Phe Asp Ser Tyr Asn Met Lys His Ile His Pro His Met	260	265	270		
Asn Met Asp Gly Asp Tyr Ile Asn Ile Phe Pro Lys Arg Lys Ala Ala	275	280	285		
Tyr Asp Ser Asn Gly Asn Val Ala Val Ala Phe Leu Tyr Tyr Lys Ser	290	295	300		
Ile Gly Pro Leu Leu Ser Ser Ser Asp Asn Phe Leu Leu Lys Pro Gln	305	310	315		320
Asn Tyr Asp Asn Ser Glu Glu Glu Glu Arg Val Ile Ser Ser Val Ile	325	330	335		
Ser Val Ser Met Ser Ser Asn Pro Pro Thr Leu Tyr Glu Leu Glu Lys	340	345	350		
Ile Thr Phe Thr Leu Ser His Arg Lys Val Thr Asp Arg Tyr Arg Ser	355	360	365		
Leu Cys Ala Phe Trp Asn Tyr Ser Pro Asp Thr Met Asn Gly Ser Trp	370	375	380		
Ser Ser Glu Gly Cys Glu Leu Thr Tyr Ser Asn Glu Thr His Thr Ser	385	390	395		400
Cys Arg Cys Asn His Leu Thr His Phe Ala Ile Leu Met Ser Ser Gly	405	410	415		
Pro Ser Ile Gly Ile Lys Asp Tyr Asn Ile Leu Thr Arg Ile Thr Gln	420	425	430		
Leu Gly Ile Ile Ile Ser Leu Ile Cys Leu Ala Ile Cys Ile Phe Thr	435	440	445		
Phe Trp Phe Phe Ser Glu Ile Gln Ser Thr Arg Thr Thr Ile His Lys	450	455	460		

0909320 "071801

Asn Leu Cys Cys Ser Leu Phe Leu Ala Glu Leu Val Phe Leu Val Gly  
 465 470 475 480  
 Ile Asn Thr Asn Thr Asn Lys Leu Phe Cys Ser Ile Ile Ala Gly Leu  
 485 490 495  
 Leu His Tyr Phe Phe Leu Ala Ala Phe Ala Trp Met Cys Ile Glu Gly  
 500 505 510  
 Ile His Leu Tyr Leu Ile Val Val Gly Val Ile Tyr Asn Lys Gly Phe  
 515 520 525  
 Leu His Lys Asn Phe Tyr Ile Phe Gly Tyr Leu Ser Pro Ala Val Val  
 530 535 540  
 Val Gly Phe Ser Ala Ala Leu Gly Tyr Arg Tyr Tyr Gly Thr Thr Lys  
 545 550 555 560  
 Val Cys Trp Leu Ser Thr Glu Asn Asn Phe Ile Trp Ser Phe Ile Gly  
 565 570 575  
 Pro Ala Cys Leu Ile Ile Leu Val Asn Leu Leu Ala Phe Gly Val Ile  
 580 585 590  
 Ile Tyr Lys Val Phe Arg His Thr Ala Gly Leu Lys Pro Glu Val Ser  
 595 600 605  
 Cys Phe Glu Asn Ile Arg Ser Cys Ala Arg Gly Ala Leu Ala Leu Leu  
 610 615 620  
 Phe Leu Leu Gly Thr Thr Trp Ile Phe Gly Val Leu His Val Val His  
 625 630 635 640  
 Ala Ser Val Val Thr Ala Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln  
 645 650 655  
 Gly Met Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln  
 660 665 670  
 Glu Glu Tyr Tyr Arg Leu Phe Lys Asn Val Pro Cys Cys Phe Gly Cys  
 675 680 685  
 Leu Arg  
 690  
 <210> 50  
 <211> 589  
 <212> DNA  
 <213> Homo sapiens  
 <220>  
 <221> modified\_base  
 <222> (61)

0909220-071301  
 0909220-071301



<223> a, t, c or g

<400> 50

```

tggaacata tcctccctca tatgaatatg gatggagact acataaatat atttccaaag 60
ngaaaagccg gcatatggat tcaaattggca atgttgagcag tgcattttta tattataaga 120
gtattgggtcc ctttgctttc atcatctgac aacttccttat tgaaacctca aaattatgat 180
aattctgaag aggaggaaaag agtcataatct tcagtaattt cagtctcaat gagctcaaac 240
ccaccacat tatatgaact tgaaaaaata acatttacat taagtcacg aaaggtcaca 300
gataggata ggagtctatg tggcattttg gaatactcac ctgataccat gaatggcagc 360
tgggtcttcag agggctgtga gctgacatac tcaaattgaga cccacacctc atgccgctgt 420
aatcacctga cacattttgc aattttgatg tcctctgggc cttccattgg tattaaagat 480
tataatattc ttacaaggat cactcaacta ggaataatta tttcactgat ttgtcttgcc 540
atatgcattt ttaccttctg gttcttcagt gaaattcaaa gcaccagga 589

```

<210> 51

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 51

ggtaatgagc tccattacag 20

<210> 52

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 52

ggagtagaaa gcgcatgg 18

<210> 53

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 53

cacctgatac catgaatggc ag 22

<210> 54

<211> 18

<212> DNA

T08T20-02E60650

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 54

cgagctcgaa ttaattcg

18

<210> 55

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 55

ggatctcctg agctcagg

18

<210> 56

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 56

cctagttgag tgatccttgt aag

23

<210> 57

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 57

atgagacca cacctcatgc cgctgtaatc acctgacaca ttttgcaatt

50

<210> 58

<211> 2137

<212> DNA

<213> Homo sapiens

<400> 58

gctcccagcc aagaacctcg gggccgctgc gcggtgggga ggagttcccc gaaacccggc 60  
cgctaagcga ggccctcctcc tcccgcagat ccgaacggcc tgggcggggt caccgccgct 120

09909320-071301

gggacaagaa gccgcgcgct gcctgcccgg gcccggggag ggggctgggg ctggggccgg 180  
 aggcgggggtg tgagtgggtg tgtgcggggg gcggaggctt gatgcaatcc cgataagaaa 240  
 tgctcgggtg tcttggggcac ctaccgctgg ggcccgtaag gcgctactat ataaggctgc 300  
 cggccccggag ccgcgcgcgc gtcagagcag gagcgtgctg tccaggatct agggccacga 360  
 ccatcccaac ccggcactca cagccccgca gcgcatcccc gtcgcccggc agcctccccg 420  
 acccccatcg ccggagctgc gccgagagcc ccagggaggt gccatgcgga gcgggtgtgt 480  
 ggtggtccac gtatggatcc tggccggcct ctggctggcc gtggccgggc gccccctcgc 540  
 cttctcggac gcggggcccc acgtgcacta cggctggggc gaccccatcc gcctgcggca 600  
 cctgtacacc tccggcccc acgggctctc cagctgcttc ctgcgcaccc gtgccgacgg 660  
 cgtcgtggac tgcgcgcggg gccagagcgc gcacagtctg ctggagatca aggcagtcgc 720  
 tctgcggacc gtggccatca agggcgctgca cagcgtgctg tacctctgca tgggcgcga 780  
 cggcaagatg caggggctgc ttcagtactc ggaggaagac tgtgctttcg aggaggagat 840  
 ccgcccagat ggctacaatg tgtaccgatc cgagaagcac cgctccccg tctccctgag 900  
 cagtgccaaa cagcggcagc tgtacaagaa cagaggcttt cttccactct ctcatttcct 960  
 gcccatgctg cccatggtcc cagaggagcc tgaggacctc agggggcact tggaatctga 1020  
 catgttctct tcgccccctg agaccgacag catggacca tttgggcttg tcaccggact 1080  
 ggaggccgtg aggagtccca gctttgagaa gtaactgaga ccatgcccgg gcctcttcac 1140  
 tgctgccagg ggctgtggta cctgcagcgt gggggacgtg cttctacaag aacagtcctg 1200  
 agtccacggt ctgttttagct ttaggaagaa acatctagaa gttgtacata ttcagagttt 1260  
 tccattggca gtgccagttt ctagccaata gacttgtctg atcataacat tgtaagcctg 1320  
 tagcttgccc agctgctgcc tgggccccca ttctgctccc tcgagggtgc tggacaagct 1380  
 gctgcaactgt ctcaagctg cttgaatacc tccatcgatg gggaactcac ttcctttgga 1440  
 aaaattctta tgtcaagctg aaattctcta atttttctc atcacttccc caggagcagc 1500  
 cagaagacag gcagtagttt taatttcagg aacaggtgat ccactctgta aaacagcagg 1560  
 taaatttcac tcaaccccat gtgggaattg atctatatct ctacttccag ggaccatttg 1620  
 cccttcccaa atccctccag gccagaactg actggagcag gcatggccca ccaggcttca 1680  
 ggagtagggg aagcctggag cccactcca gccctgggac aacttgagaa ttccccctga 1740  
 ggccagttct gtcatggatg ctgtcctgag aataacttgc tgtcccggtg tcacctgctt 1800  
 ccatctccca gccaccagc cctctgcccc cctcacatgc ctccccatgg attggggcct 1860  
 cccaggcccc ccaccttatg tcaacctgca cttcttggtc aaaaatcagg aaaagaaaag 1920  
 atttgaagac cccaagtctt gtcaataact tgctgtgtgg aagcagcggg ggaagaccta 1980  
 gaacctttc cccagcactt ggttttccaa catgatattt atgagtaatt tattttgata 2040  
 tgtacatctc ttattttctt acattattta tgccccaaa ttatatttat gtatgtaagt 2100  
 gaggtttgtt ttgtatatta aaatggagtt tgtttgt 2137

<210> 59

<211> 216

<212> PRT

<213> Homo sapiens

<400> 59

Met Arg Ser Gly Cys Val Val Val His Val Trp Ile Leu Ala Gly Leu  
 1 5 10 15

Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro  
 20 25 30

His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr  
 35 40 45

Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala  
 50 55 60

Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser Ala His Ser Leu Leu  
 65 70 75 80  
 Glu Ile Lys Ala Val Ala Leu Arg Thr Val Ala Ile Lys Gly Val His  
 85 90 95  
 Ser Val Arg Tyr Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu  
 100 105 110  
 Leu Gln Tyr Ser Glu Glu Asp Cys Ala Phe Glu Glu Glu Ile Arg Pro  
 115 120 125  
 Asp Gly Tyr Asn Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser  
 130 135 140  
 Leu Ser Ser Ala Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu  
 145 150 155 160  
 Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro  
 165 170 175  
 Glu Asp Leu Arg Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu  
 180 185 190  
 Glu Thr Asp Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala  
 195 200 205  
 Val Arg Ser Pro Ser Phe Glu Lys  
 210 215

&lt;210&gt; 60

&lt;211&gt; 26

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 60

atccgccag atggctacaa tgtgta

26

&lt;210&gt; 61

&lt;211&gt; 42

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 61

gcctcccggt ctccctgagc agtgccaaac agcggcagtg ta

42

T03T20"07E0660

<210> 62  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 62  
 ccagtccggt gacaagccca aa 22

<210> 63  
 <211> 1295  
 <212> DNA  
 <213> Homo sapiens

<400> 63  
 cccagaagtt caagggcccc cggcctcctg cgctcctgcc gccgggaccc tcgacctcct 60  
 cagagcagcc ggctgccgcc ccgggaagat ggcgaggagg agccgccacc gcctcctcct 120  
 gctgctgctg cgctacctgg tggcgccctt gggctatcat aaggcctatg ggttttctgc 180  
 cccaaaagac caacaagtag tcacagcagt agagtaccaa gaggtatatt tagcctgcaa 240  
 aaccccaaag aagactgttt cctccagatt agagtggaaag aaactgggtc ggagtgtctc 300  
 ctttgtctac tatcaacaga ctcttcaagg tgattttaaa aatcgagctg agatgataga 360  
 tttcaatata cggatcaaaa atgtgacaag aagtgatgcg gggaaatatc gttgtgaagt 420  
 tagtgcccca tctgagcaag gccaaaacct ggaagaggat acagtactc tggaaagtatt 480  
 agtggtccca gcagttccat catgtgaagt accctcttct gctctgagtg gaactgtggt 540  
 agagctacga tgtcaagaca aagaaggga tccagctcct gaatacacat ggtttaagga 600  
 tggcatccgt ttgctagaaa atcccagact tggctcccaa agcaccaaca gctcatacac 660  
 aatgaatata aaaactggaa ctctgcaatt taatactgtt tccaaactgg acactggaga 720  
 atattcctgt gaagcccgcga attctgttgg atatcgaggg tgctctggga aacgaatgca 780  
 agtagatgat ctcaacataa gtggcatcat agcagccgta gtagttgtgg ccttagtgat 840  
 ttccgtttgt ggcttgggtg tatgctatgc tcagaggaaa ggctactttt caaaagaaac 900  
 ctcttccag aagagtaatt ctctcatctaa agccacgaca atgagtgaat atgtgcagtg 960  
 gctcacgctt gtaatccag cactttggaa ggccgcggcg ggcggatcac gaggtcagga 1020  
 gttctagacc agtctggcca atatggtgaa accccatctc tactaaaata caaaaattag 1080  
 ctgggcatgg tggcatgtgc ctgcagttcc agctgcttgg gagacaggag aatcacttga 1140  
 acccgggagg cggagggtgc agtgagctga gatcacgcca ctgcagtcca gcctgggtaa 1200  
 cagagcaaga ttccatctca aaaaataaaa taaataaata aataaatact ggtttttacc 1260  
 tgtagaattc ttacaataaa tatagcttga tattc 1295

<210> 64  
 <211> 312  
 <212> PRT  
 <213> Homo sapiens

<400> 64  
 Met Ala Arg Arg Ser Arg His Arg Leu Leu Leu Leu Leu Arg Tyr  
 1 5 10 15  
 Leu Val Val Ala Leu Gly Tyr His Lys Ala Tyr Gly Phe Ser Ala Pro  
 20 25 30

0909320.071301

Lys	Asp	Gln	Gln	Val	Val	Thr	Ala	Val	Glu	Tyr	Gln	Glu	Ala	Ile	Leu
35						40						45			
Ala	Cys	Lys	Thr	Pro	Lys	Lys	Thr	Val	Ser	Ser	Arg	Leu	Glu	Trp	Lys
50						55				60					
Lys	Leu	Gly	Arg	Ser	Val	Ser	Phe	Val	Tyr	Tyr	Gln	Gln	Thr	Leu	Gln
65				70				75						80	
Gly	Asp	Phe	Lys	Asn	Arg	Ala	Glu	Met	Ile	Asp	Phe	Asn	Ile	Arg	Ile
				85				90						95	
Lys	Asn	Val	Thr	Arg	Ser	Asp	Ala	Gly	Lys	Tyr	Arg	Cys	Glu	Val	Ser
		100						105				110			
Ala	Pro	Ser	Glu	Gln	Gly	Gln	Asn	Leu	Glu	Glu	Asp	Thr	Val	Thr	Leu
115						120						125			
Glu	Val	Leu	Val	Ala	Pro	Ala	Val	Pro	Ser	Cys	Glu	Val	Pro	Ser	Ser
130						135				140					
Ala	Leu	Ser	Gly	Thr	Val	Val	Glu	Leu	Arg	Cys	Gln	Asp	Lys	Glu	Gly
145				150						155				160	
Asn	Pro	Ala	Pro	Glu	Tyr	Thr	Trp	Phe	Lys	Asp	Gly	Ile	Arg	Leu	Leu
				165				170						175	
Glu	Asn	Pro	Arg	Leu	Gly	Ser	Gln	Ser	Thr	Asn	Ser	Ser	Tyr	Thr	Met
		180						185				190			
Asn	Thr	Lys	Thr	Gly	Thr	Leu	Gln	Phe	Asn	Thr	Val	Ser	Lys	Leu	Asp
195						200						205			
Thr	Gly	Glu	Tyr	Ser	Cys	Glu	Ala	Arg	Asn	Ser	Val	Gly	Tyr	Arg	Arg
210						215				220					
Cys	Pro	Gly	Lys	Arg	Met	Gln	Val	Asp	Asp	Leu	Asn	Ile	Ser	Gly	Ile
225				230				235						240	
Ile	Ala	Ala	Val	Val	Val	Val	Ala	Leu	Val	Ile	Ser	Val	Cys	Gly	Leu
				245				250						255	
Gly	Val	Cys	Tyr	Ala	Gln	Arg	Lys	Gly	Tyr	Phe	Ser	Lys	Glu	Thr	Ser
		260						265				270			
Phe	Gln	Lys	Ser	Asn	Ser	Ser	Ser	Lys	Ala	Thr	Thr	Met	Ser	Glu	Asn
275						280						285			
Val	Gln	Trp	Leu	Thr	Pro	Val	Ile	Pro	Ala	Leu	Trp	Lys	Ala	Ala	Ala
290						295				300					
Gly	Gly	Ser	Arg	Gly	Gln	Glu	Phe								

305 310

<210> 65  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 65  
 atcgttgtga agttagtgcc cc 22

<210> 66  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 66  
 acctgcgata tccaacagaa ttg 23

<210> 67  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 67  
 ggaagaggat acagtcactc tggaagtatt agtggctcca gcagttcc 48

<210> 68  
 <211> 2639  
 <212> DNA  
 <213> Homo sapiens

<400> 68  
 gacatcggag gtgggctagc actgaaactg cttttcaaga cgaggaagag gaggagaaaag 60  
 agaaagaaga ggaagatggt gggcaacatt tatttaacat gctccacagc ccggaccctg 120  
 gcatcatgct gctattcctg caaatactga agaagcatgg gatttaaata ttttacttct 180  
 aaataaatga attactcaat ctccatgac catctatata tactccacct tcaaaaagta 240  
 catcaatatt atatcattaa ggaaatagta accttctctt ctccaatatg catgacattt 300  
 ttggacaatg caattgtggc actggcactt atttcagtga agaaaaactt tgtggttcta 360  
 tggcattcat catttgacaa atgcaagcat cttccttatc aatcagctcc tattgaactt 420  
 actagcactg actgtggaat ccttaagggc ccattacatt tctgaagaag aaagctaaga 480  
 tgaaggacat gccactccga attcatgtgc tacttggcct agctatcact acactagtac 540

0909320 071801

aagctgtaga taaaaaagtg gattgtccac gggtatgtac gtgtgaaatc aggccttggt 600  
ttacacccag atccatttat atggaagcat ctacagtga ttgtaatgat ttaggtcttt 660  
taactttccc agccagattg ccagctaaca cacagattct tctcctacag actaacaata 720  
ttgcaaaaat tgaatactcc acagactttc cagtaaacct tactggcctg gatttatctc 780  
aaaacaattt atcttcagtc accaatatta atgtaaaaaa gatgcctcag ctccctttctg 840  
tgtacctaga ggaaaacaaa cttactgaac tgcctgaaaa atgtctgtcc gaactgagca 900  
acttacaaga actctatatt aatcacaact tgctttctac aatttcacct ggagccttta 960  
ttggcctaca taatcttctt cgacttcac tcaattcaaa tagattgcag atgatcaaca 1020  
gtaagtgggt tgatgctctt ccaaattctag agattctgat gattggggaa aatccaatta 1080  
tcagaatcaa agacatgaac tttaagcctc ttatcaatct tcgcagcctg gttatagctg 1140  
gtataaacct cacagaaata ccagataacg ccttggttgg actggaaaac ttagaaaagca 1200  
tctcttttta cgataacagg cttattaaag taccctcatgt tgctcttcaa aaagttgtaa 1260  
atctcaaatt tttggatcta aataaaaaat ctattaatag aatacgaagg ggtgatttta 1320  
gcaatatgct acacttaaaa gagttgggga taaataatat gcctgagctg atttccatcg 1380  
atagtcttgc tgtggataac ctgccagatt taagaaaaat agaagctact aacaacccta 1440  
gattgtctta cattcacccc aatgcatttt tcagactccc caagctggaa tcactcatgc 1500  
tgaacagcaa tgctctcagt gccctgtacc atgggtaccat tgagtctctg ccaaacctca 1560  
aggaaatcag catacacagt aaccccatca ggtgtgactg tgtcatccgt tggatgaaca 1620  
tgaacaaaac caacattcga ttcatggagc cagattcact gttttgcgtg gaccacctg 1680  
aattccaagg tcagaatgtt cggcaagtgc atttcaggga catgatggaa atttgtctcc 1740  
ctcttatagc tctgagagc tttccttcta atctaaatgt agaagctggg agctatgttt 1800  
cctttcactg tagagctact gcagaaccac agcctgaaat ctactggata acaccttctg 1860  
gtcaaaaact cttgcctaact accctgacag acaagttcta tgtccattct gagggaaacac 1920  
tagatataaa tggcgtaact cccaaagaag ggggtttata tacttgata gcaactaacc 1980  
tagttggcgc tgacttgaag tctgttatga tcaaagtga tggatctttt ccacaagata 2040  
acaatggctc tttgaatatt aaaataagag atattcaggc caattcagtt ttggtgtcct 2100  
ggaaagcaag ttctaaaatt ctcaaacta gtgttaaag gacagccttt gtcaagactg 2160  
aaaattctca tgctgcgcaa agtgctcgaa taccatctga tgtcaaggta tataatctta 2220  
ctcatctgaa tccatcaact gagtataaaa tttgtattga tattcccacc atctatcaga 2280  
aaaacagaaa aaaatgtgta aatgtcacca ccaaagggtt gcaccctgat caaaaagagt 2340  
atgaaaagaa taataccaca acacttatgg cctgtcttgg aggccttctg gggattattg 2400  
gtgtgatatg tcttatcagc tgcctctctc cagaaatgaa ctgtgatggg ggacacagct 2460  
atgtgaggaa ttacttacag aaaccaacct ttgcattagg tgagctttat cctcctctga 2520  
taaattctctg ggaagcagga aaagaaaaaa gtacatcact gaaagtaaaa gcaactgtta 2580  
taggtttacc aacaaatatg tcctaaaaac caccaaggaa acctactcca aaaatgaac 2639

<210> 69

<211> 708

<212> PRT

<213> Homo sapiens

<400> 69

Met Lys Asp Met Pro Leu Arg Ile His Val Leu Leu Gly Leu Ala Ile  
1 5 10 15

Thr Thr Leu Val Gln Ala Val Asp Lys Lys Val Asp Cys Pro Arg Leu  
20 25 30

Cys Thr Cys Glu Ile Arg Pro Trp Phe Thr Pro Arg Ser Ile Tyr Met  
35 40 45

Glu Ala Ser Thr Val Asp Cys Asn Asp Leu Gly Leu Leu Thr Phe Pro  
50 55 60

FOOTNOTES



Ala Arg Leu Pro Ala Asn Thr Gln Ile Leu Leu Leu Gln Thr Asn Asn  
 65 70 75 80  
 Ile Ala Lys Ile Glu Tyr Ser Thr Asp Phe Pro Val Asn Leu Thr Gly  
 85 90 95  
 Leu Asp Leu Ser Gln Asn Asn Leu Ser Ser Val Thr Asn Ile Asn Val  
 100 105 110  
 Lys Lys Met Pro Gln Leu Leu Ser Val Tyr Leu Glu Glu Asn Lys Leu  
 115 120 125  
 Thr Glu Leu Pro Glu Lys Cys Leu Ser Glu Leu Ser Asn Leu Gln Glu  
 130 135 140  
 Leu Tyr Ile Asn His Asn Leu Leu Ser Thr Ile Ser Pro Gly Ala Phe  
 145 150 155 160  
 Ile Gly Leu His Asn Leu Leu Arg Leu His Leu Asn Ser Asn Arg Leu  
 165 170 175  
 Gln Met Ile Asn Ser Lys Trp Phe Asp Ala Leu Pro Asn Leu Glu Ile  
 180 185 190  
 Leu Met Ile Gly Glu Asn Pro Ile Ile Arg Ile Lys Asp Met Asn Phe  
 195 200 205  
 Lys Pro Leu Ile Asn Leu Arg Ser Leu Val Ile Ala Gly Ile Asn Leu  
 210 215 220  
 Thr Glu Ile Pro Asp Asn Ala Leu Val Gly Leu Glu Asn Leu Glu Ser  
 225 230 235 240  
 Ile Ser Phe Tyr Asp Asn Arg Leu Ile Lys Val Pro His Val Ala Leu  
 245 250 255  
 Gln Lys Val Val Asn Leu Lys Phe Leu Asp Leu Asn Lys Asn Pro Ile  
 260 265 270  
 Asn Arg Ile Arg Arg Gly Asp Phe Ser Asn Met Leu His Leu Lys Glu  
 275 280 285  
 Leu Gly Ile Asn Asn Met Pro Glu Leu Ile Ser Ile Asp Ser Leu Ala  
 290 295 300  
 Val Asp Asn Leu Pro Asp Leu Arg Lys Ile Glu Ala Thr Asn Asn Pro  
 305 310 315 320  
 Arg Leu Ser Tyr Ile His Pro Asn Ala Phe Phe Arg Leu Pro Lys Leu  
 325 330 335  
 Glu Ser Leu Met Leu Asn Ser Asn Ala Leu Ser Ala Leu Tyr His Gly

0909320-01801

340	345	350
Thr Ile Glu Ser Leu Pro Asn Leu Lys Glu Ile Ser Ile His Ser Asn		
355	360	365
Pro Ile Arg Cys Asp Cys Val Ile Arg Trp Met Asn Met Asn Lys Thr		
370	375	380
Asn Ile Arg Phe Met Glu Pro Asp Ser Leu Phe Cys Val Asp Pro Pro		
385	390	395
Glu Phe Gln Gly Gln Asn Val Arg Gln Val His Phe Arg Asp Met Met		
405	410	415
Glu Ile Cys Leu Pro Leu Ile Ala Pro Glu Ser Phe Pro Ser Asn Leu		
420	425	430
Asn Val Glu Ala Gly Ser Tyr Val Ser Phe His Cys Arg Ala Thr Ala		
435	440	445
Glu Pro Gln Pro Glu Ile Tyr Trp Ile Thr Pro Ser Gly Gln Lys Leu		
450	455	460
Leu Pro Asn Thr Leu Thr Asp Lys Phe Tyr Val His Ser Glu Gly Thr		
465	470	475
Leu Asp Ile Asn Gly Val Thr Pro Lys Glu Gly Gly Leu Tyr Thr Cys		
485	490	495
Ile Ala Thr Asn Leu Val Gly Ala Asp Leu Lys Ser Val Met Ile Lys		
500	505	510
Val Asp Gly Ser Phe Pro Gln Asp Asn Asn Gly Ser Leu Asn Ile Lys		
515	520	525
Ile Arg Asp Ile Gln Ala Asn Ser Val Leu Val Ser Trp Lys Ala Ser		
530	535	540
Ser Lys Ile Leu Lys Ser Ser Val Lys Trp Thr Ala Phe Val Lys Thr		
545	550	555
Glu Asn Ser His Ala Ala Gln Ser Ala Arg Ile Pro Ser Asp Val Lys		
565	570	575
Val Tyr Asn Leu Thr His Leu Asn Pro Ser Thr Glu Tyr Lys Ile Cys		
580	585	590
Ile Asp Ile Pro Thr Ile Tyr Gln Lys Asn Arg Lys Lys Cys Val Asn		
595	600	605
Val Thr Thr Lys Gly Leu His Pro Asp Gln Lys Glu Tyr Glu Lys Asn		
610	615	620

09909320.071801

Asn Thr Thr Thr Leu Met Ala Cys Leu Gly Gly Leu Leu Gly Ile Ile  
625 630 635 640

Gly Val Ile Cys Leu Ile Ser Cys Leu Ser Pro Glu Met Asn Cys Asp  
645 650 655

Gly Gly His Ser Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala  
660 665 670

Leu Gly Glu Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys  
675 680 685

Glu Lys Ser Thr Ser Leu Lys Val Lys Ala Thr Val Ile Gly Leu Pro  
690 695 700

Thr Asn Met Ser  
705

<210> 70  
<211> 1305  
<212> DNA  
<213> Homo sapiens

<400> 70  
gcccgggact ggcgcaagggt gcccaagcaa ggaaagaaat aatgaagaga cacatgtggt 60  
agctgcagcc ttttgaaaca cgcaagaagg aaatcaatag tgtggacagg gctggaacct 120  
ttaccacgct tgttgagta gatgaggaat gggtcgtga ttatgctgac attccagcat 180  
gaatctggta gacctgtggt taaccggttc cctctccatg tgtctcctcc taaaaagttt 240  
tggtcttatg atactgtgct ttcattctgc cagtatgtgt cccaagggct gtctttgttc 300  
ttcctctggg ggtttaaatg tcacctgtag caatgcaaat ctcaaggaaa tacctagaga 360  
tcttctcct gaaacagtct tactgtatct ggactccaat cagatcacat ctattcccaa 420  
tgaaatTTTT aaggacctcc atcaactgag agttctcaac ctgtccaaaa atggcattga 480  
gtttatcgat gagcatgcct tcaaaggagt agctgaaacc ttgcagactc tggacttgct 540  
cgacaatcgg attcaaagtg tgcacaaaaa tgccttcaat aacctgaagg ccagggccag 600  
aattgccaac aacctctggc actgcgactg tactctacag caagttctga ggagcatggc 660  
gtccaatcat gagacagccc acaacgtgat ctgtaaaacg tccgtgttg atgaacatgc 720  
tggcagacca ttctcaatg ctgccaacga cgtgacctt tgtaacctcc ctaaaaaaac 780  
taccgattat gccatgctgg tcacctgtt tggctgggtc actatggtga tctcatatgt 840  
ggtatattat gtgaggcaaa atcaggagga tgcccggaga cacctcgaat acttgaaatc 900  
cctgccaaagc aggcagaaga aagcagatga acctgatgat attagcactg tggatatagt 960  
tccaaactga ctgtcattga gaaagaaaga aagtagtttg cgattgcagt agaaataagt 1020  
ggtttacttc tcccatccat tgtaaacatt tgaaactttg tatttcagtt ttttttgaat 1080  
tatgccactg ctgaactttt aacaaacact acaacataaa taatttgagt ttaggtgatc 1140  
cacccttaa ttgtaccccc gatggtatat ttctgagtaa gctactatct gaacattagt 1200  
tagatccatc tcaactatta ataatgaaat ttattttttt aattttaaag caaataaaag 1260  
cttaactttg aaccatggga aaaaaaaaaa aaaaaaaaaa aaaca 1305

<210> 71  
<211> 259  
<212> PRT  
<213> Homo sapiens

<400> 71

0909320-0401

Met Asn Leu Val Asp Leu Trp Leu Thr Arg Ser Leu Ser Met Cys Leu  
 1 5 10 15  
 Leu Leu Gln Ser Phe Val Leu Met Ile Leu Cys Phe His Ser Ala Ser  
 20 25 30  
 Met Cys Pro Lys Gly Cys Leu Cys Ser Ser Ser Gly Gly Leu Asn Val  
 35 40 45  
 Thr Cys Ser Asn Ala Asn Leu Lys Glu Ile Pro Arg Asp Leu Pro Pro  
 50 55 60  
 Glu Thr Val Leu Leu Tyr Leu Asp Ser Asn Gln Ile Thr Ser Ile Pro  
 65 70 75 80  
 Asn Glu Ile Phe Lys Asp Leu His Gln Leu Arg Val Leu Asn Leu Ser  
 85 90 95  
 Lys Asn Gly Ile Glu Phe Ile Asp Glu His Ala Phe Lys Gly Val Ala  
 100 105 110  
 Glu Thr Leu Gln Thr Leu Asp Leu Ser Asp Asn Arg Ile Gln Ser Val  
 115 120 125  
 His Lys Asn Ala Phe Asn Asn Leu Lys Ala Arg Ala Arg Ile Ala Asn  
 130 135 140  
 Asn Pro Trp His Cys Asp Cys Thr Leu Gln Gln Val Leu Arg Ser Met  
 145 150 155 160  
 Ala Ser Asn His Glu Thr Ala His Asn Val Ile Cys Lys Thr Ser Val  
 165 170 175  
 Leu Asp Glu His Ala Gly Arg Pro Phe Leu Asn Ala Ala Asn Asp Ala  
 180 185 190  
 Asp Leu Cys Asn Leu Pro Lys Lys Thr Thr Asp Tyr Ala Met Leu Val  
 195 200 205  
 Thr Met Phe Gly Trp Phe Thr Met Val Ile Ser Tyr Val Val Tyr Tyr  
 210 215 220  
 Val Arg Gln Asn Gln Glu Asp Ala Arg Arg His Leu Glu Tyr Leu Lys  
 225 230 235 240  
 Ser Leu Pro Ser Arg Gln Lys Lys Ala Asp Glu Pro Asp Asp Ile Ser  
 245 250 255  
 Thr Val Val

<210> 72  
 <211> 2290

FOOTNOTES

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 72

```

accgagccga gcggaaccgaa ggcgcgcccc agatgcaggt gagcaagagg atgctggcgg 60
ggggcgtgag gagcatgccc agccccctcc tggcctgctg gcagcccatc ctctgctgg 120
tgctgggctc agtgctgtca ggctcggcca cgggctgccc gccccgctgc gagtgtccg 180
cccaggaccg cgctgtgctg tgccaccgca agtgctttgt ggcagtcccc gagggcatcc 240
ccaccgagac gcgcctgctg gacctaggca agaaccgcat caaaacgctc aaccaggacg 300
agttcgccag cttcccgcac ctggaggagc tggagctcaa cgagaacatc gtgagcgccg 360
tggagccccg cgccctcaac aacctcttca acctccggac gctgggtctc cgcagcaacc 420
gcctgaagct catcccgcta ggcgtcttca ctggcctcag caacctgacc aagcaggaca 480
tcagcgagaa caagatcggt atcctaactg actacatgtt tcaggacctg tacaacctca 540
agtcactgga ggttggcgac aatgacctcg tctacatctc tcaccgcgcc ttcagcggcc 600
tcaacagcct ggagcagctg acgctggaga aatgcaacct gacctccatc cccaccgagg 660
cgctgtccca cctgcacggc ctcatcgctc tgaggctccg gcacctcaac atcaatgcca 720
tccgggacta ctccctcaag aggctgtacc gactcaaggc cttggagatc tccactggc 780
cctacttgga caccatgaca cccaactgcc tctacggcct caacctgacg tccctgtcca 840
tcacacactg caatctgacc gctgtgccct acctggccgt ccgccacctt gtctatctcc 900
gcttctcaa cctctctac aaccccatca gcaccattga gggctccatg ttgcatgagc 960
tgctccggct gcaggagatc cagctgggtg gcgggcagct ggccgtggtg gagccctatg 1020
ccttccgcgg cctcaactac ctgcgcgtgc tcaatgtctc tggcaaccag ctgaccacac 1080
tggaggaatc agtcttccac tcgggtggga acctggagac actcatcctg gactccaacc 1140
cgctggcctg cgactgtcgg ctctgtgagg tgttccggcg ccgctggcggt ctcaacttca 1200
accggagca gccacgtgc gccacgcccg agtttgtcca gggcaaggag ttcaaggact 1260
tccctgatgt gctactgccc aactacttca cctgccggcg cggccgcatc cgggaccgca 1320
aggcccagca ggtgtttgtg gacgagggcc acacgggtgca gtttgtgtgc cgggcccgatg 1380
gcgaccgcc gcccgccatc ctctggctct caccgccaaa gcacctggtc tcagccaaga 1440
gcaatgggcg gctcacagtc ttcctgatg gcacgctgga ggtgcgctac gcccaggtac 1500
aggacaacgg cacgtacctg tgcacgcgg ccaacgcggg cggcaacgac tccatgcccg 1560
cccacctgca tgtgcgcagc tactcgcccg actggcccca tcagcccaac aagaccttcg 1620
ctttcatctc caaccagccg ggcgagggag agggcaacag caccgcgcc actgtgcctt 1680
tccccttoga catcaagacc ctcatcatcg ccaccacctt gggcttcatc tctttcctgg 1740
gcgtcgtcct cttctgcctg gtgctgctgt ttctctggag ccggggcaag ggcaacacaa 1800
agcacaacat cgagatcgag tatgtgcccc gaaagtgcga cgcaggcatc agctccgccg 1860
acgcgccccg caagttcaac atgaagatga tatgaggccg gggcgggggg cagggacccc 1920
cgggcggccg ggcaggggaa ggggcctggt cgccacctgc tcaacttcca gtccctccca 1980
cctcctcctt acccttctac acacgttctc tttctccctc ccgcctcgt cccctgctgc 2040
cccccgccag cctcaccac ctgccctcct tctaccagga cctcagaagc ccagacctgg 2100
ggacccacc tacacagggg cattgacaga ctggagtga aagccgacga accgacacgc 2160
ggcagagtca ataattcaat aaaaaagtta cgaactttct ctgtaacttg ggtttcaata 2220
attatggatt tttatgaaaa cttgaaataa taaaaagaga aaaaaactaa aaaaaaaaaa 2280
aaaaaaaaaa 2290

```

&lt;210&gt; 73

&lt;211&gt; 620

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 73

Met Gln Val Ser Lys Arg Met Leu Ala Gly Gly Val Arg Ser Met Pro

1

5

10

15

F03F20/02E60650

Ser Pro Leu Leu Ala Cys Trp Gln Pro Ile Leu Leu Leu Val Leu Gly  
 20 25 30  
 Ser Val Leu Ser Gly Ser Ala Thr Gly Cys Pro Pro Arg Cys Glu Cys  
 35 40 45  
 Ser Ala Gln Asp Arg Ala Val Leu Cys His Arg Lys Cys Phe Val Ala  
 50 55 60  
 Val Pro Glu Gly Ile Pro Thr Glu Thr Arg Leu Leu Asp Leu Gly Lys  
 65 70 75 80  
 Asn Arg Ile Lys Thr Leu Asn Gln Asp Glu Phe Ala Ser Phe Pro His  
 85 90 95  
 Leu Glu Glu Leu Glu Leu Asn Glu Asn Ile Val Ser Ala Val Glu Pro  
 100 105 110  
 Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg Thr Leu Gly Leu Arg Ser  
 115 120 125  
 Asn Arg Leu Lys Leu Ile Pro Leu Gly Val Phe Thr Gly Leu Ser Asn  
 130 135 140  
 Leu Thr Lys Gln Asp Ile Ser Glu Asn Lys Ile Val Ile Leu Leu Asp  
 145 150 155 160  
 Tyr Met Phe Gln Asp Leu Tyr Asn Leu Lys Ser Leu Glu Val Gly Asp  
 165 170 175  
 Asn Asp Leu Val Tyr Ile Ser His Arg Ala Phe Ser Gly Leu Asn Ser  
 180 185 190  
 Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn Leu Thr Ser Ile Pro Thr  
 195 200 205  
 Glu Ala Leu Ser His Leu His Gly Leu Ile Val Leu Arg Leu Arg His  
 210 215 220  
 Leu Asn Ile Asn Ala Ile Arg Asp Tyr Ser Phe Lys Arg Leu Tyr Arg  
 225 230 235 240  
 Leu Lys Val Leu Glu Ile Ser His Trp Pro Tyr Leu Asp Thr Met Thr  
 245 250 255  
 Pro Asn Cys Leu Tyr Gly Leu Asn Leu Thr Ser Leu Ser Ile Thr His  
 260 265 270  
 Cys Asn Leu Thr Ala Val Pro Tyr Leu Ala Val Arg His Leu Val Tyr  
 275 280 285  
 Leu Arg Phe Leu Asn Leu Ser Tyr Asn Pro Ile Ser Thr Ile Glu Gly  
 290 295 300

T08F20"02E6060

Ser Met Leu His Glu Leu Leu Arg Leu Gln Glu Ile Gln Leu Val Gly  
 305 310 315 320  
 Gly Gln Leu Ala Val Val Glu Pro Tyr Ala Phe Arg Gly Leu Asn Tyr  
 325 330 335  
 Leu Arg Val Leu Asn Val Ser Gly Asn Gln Leu Thr Thr Leu Glu Glu  
 340 345 350  
 Ser Val Phe His Ser Val Gly Asn Leu Glu Thr Leu Ile Leu Asp Ser  
 355 360 365  
 Asn Pro Leu Ala Cys Asp Cys Arg Leu Leu Trp Val Phe Arg Arg Arg  
 370 375 380  
 Trp Arg Leu Asn Phe Asn Arg Gln Gln Pro Thr Cys Ala Thr Pro Glu  
 385 390 395 400  
 Phe Val Gln Gly Lys Glu Phe Lys Asp Phe Pro Asp Val Leu Leu Pro  
 405 410 415  
 Asn Tyr Phe Thr Cys Arg Arg Ala Arg Ile Arg Asp Arg Lys Ala Gln  
 420 425 430  
 Gln Val Phe Val Asp Glu Gly His Thr Val Gln Phe Val Cys Arg Ala  
 435 440 445  
 Asp Gly Asp Pro Pro Pro Ala Ile Leu Trp Leu Ser Pro Arg Lys His  
 450 455 460  
 Leu Val Ser Ala Lys Ser Asn Gly Arg Leu Thr Val Phe Pro Asp Gly  
 465 470 475 480  
 Thr Leu Glu Val Arg Tyr Ala Gln Val Gln Asp Asn Gly Thr Tyr Leu  
 485 490 495  
 Cys Ile Ala Ala Asn Ala Gly Gly Asn Asp Ser Met Pro Ala His Leu  
 500 505 510  
 His Val Arg Ser Tyr Ser Pro Asp Trp Pro His Gln Pro Asn Lys Thr  
 515 520 525  
 Phe Ala Phe Ile Ser Asn Gln Pro Gly Glu Gly Glu Ala Asn Ser Thr  
 530 535 540  
 Arg Ala Thr Val Pro Phe Pro Phe Asp Ile Lys Thr Leu Ile Ile Ala  
 545 550 555 560  
 Thr Thr Met Gly Phe Ile Ser Phe Leu Gly Val Val Leu Phe Cys Leu  
 565 570 575  
 Val Leu Leu Phe Leu Trp Ser Arg Gly Lys Gly Asn Thr Lys His Asn

0909320-071801

580

585

590

Ile Glu Ile Glu Tyr Val Pro Arg Lys Ser Asp Ala Gly Ile Ser Ser  
 595 600 605

Ala Asp Ala Pro Arg Lys Phe Asn Met Lys Met Ile  
 610 615 620

&lt;210&gt; 74

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 74

tcacctggag cctttattgg cc

22

&lt;210&gt; 75

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 75

ataccagcta taaccaggct gcg

23

&lt;210&gt; 76

&lt;211&gt; 52

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 76

caacagtaag tggtttgatg ctcttccaaa tctagagatt ctgatgattg  
gg50  
52

&lt;210&gt; 77

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

T08T20"02E50660



<400> 77  
 ccatgtgtct cctcctacaa ag 22

<210> 78  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 78  
 ggggaatagat gtgatctgat tgg 23

<210> 79  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 79  
 cacctgtagc aatgcaaadc tcaaggaaat acctagagat cttcctcctg 50

<210> 80  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 80  
 agcaaccgcc tgaagctcat cc 22

<210> 81  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 81  
 aaggcgcggt gaaagatgta gacg 24

<210> 82

FOR "0" OF 000000

<211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 82  
 gactacatgt ttcaggacct gtacaacctc aagtcactgg aggttggcga 50

<210> 83  
 <211> 1685  
 <212> DNA  
 <213> Homo sapiens

<400> 83  
 cccacgcgtc cgcacctcgg ccccgggctc cgaagcggct cgggggcgcc ctttcggtca 60  
 acatcgtagt ccacccccctc cccatcccca gccccggggg attcaggctc gccagcgccc 120  
 agccagggag ccggccggga agcgcgatgg gggccccagc cgctcgtc ctgctcctgc 180  
 tcctgctgtt cgctgctgc tgggcgcccg gcggggccaa cctctcccag gacgacagcc 240  
 agccctggac atctgatgaa acagtgggtg ctggtggcac cgtggtgctc aagtgccaaag 300  
 tgaaagatca cgaggactca tccctgcaat ggtctaaccg tgctcagcag actctctact 360  
 ttggggagaa gagagccctt cgagataatc gaattcagct ggttacctct acgccccacg 420  
 agctcagcat cagcatcagc aatgtggccc tggcagacga gggcgagtac acctgctcaa 480  
 tcttcaactat gcctgtgcga actgccaagt cctcgtcac tgtgctagga attccacaga 540  
 agcccatcat cactggttat aaatcttcat tacgggaaaa agacacagcc accctaaact 600  
 gtcagtcttc tgggagcaag cctgcagccc ggctcacctg gagaaaagggt gaccaagaac 660  
 tccacggaga accaaccgcg atacaggaag atcccaatgg taaaaccttc actgtcagca 720  
 gctcggtgac attccagggtt acccgggagg atgatggggc gagcatcgtg tgctctgtga 780  
 accatgaatc tctaaaggga gctgacagat ccacctctca acgcattgaa gttttataca 840  
 caccaactgc gatgattagg ccagaccctc cccatcctcg tgagggccag aagctgttgc 900  
 tacactgtga gggtcgcggc aatccagtcc cccagcagta cctatgggag aaggagggca 960  
 gtgtgccacc cctgaagatg acccaggaga gtgccctgat ctccctttc ctcaacaaga 1020  
 gtgacagtgg cacctacggc tgcacagcca ccagcaacat gggcagctac aaggcctact 1080  
 acaccctcaa tgtaaatgac cccagtccgg tgccctcctc ctccagcacc taccacgcca 1140  
 tcatcggtgg gatcgtggct ttcattgtct tcctgctgct catcatgctc atcttccttg 1200  
 gccactactt gatccggcac aaaggaacct acctgacaca tgaggcaaaa ggctccgacg 1260  
 atgctccaga cgcggacacg gccatcatca atgcagaagg cgggcagtca ggaggggacg 1320  
 acaagaagga atatttcac tagaggcgcc tgccacttc ctgcgcccc cagggggcct 1380  
 gtggggactg ctggggccgt caccaaccgc gacttgtaga gagcaaccgc agggccgccc 1440  
 ctcccgcttg ctccccagcc cccccacccc cctgtacaga atgtctgctt tgggtgcggt 1500  
 tttgtactcg gtttggaatg gggaggaggagg agggcggggg gaggggaggg ttgccctcag 1560  
 ccctttccgt ggcttctctg catttgggtt attattattt ttgtaacaat cccaaatcaa 1620  
 atctgtctcc aggctggaga ggcaggagcc ctgggggtgag aaaagcaaaa aacaaacaaa 1680  
 aaaca 1685

<210> 84  
 <211> 398  
 <212> PRT  
 <213> Homo sapiens

<400> 84

Met 1	Gly	Ala	Pro	Ala 5	Ala	Ser	Leu	Leu	Leu 10	Leu	Leu	Leu	Leu	Phe 15	Ala
Cys	Cys	Trp	Ala 20	Pro	Gly	Gly	Ala	Asn 25	Leu	Ser	Gln	Asp	Asp 30	Ser	Gln
Pro	Trp	Thr 35	Ser	Asp	Glu	Thr	Val 40	Val	Ala	Gly	Gly	Thr 45	Val	Val	Leu
Lys	Cys 50	Gln	Val	Lys	Asp	His 55	Glu	Asp	Ser	Ser	Leu 60	Gln	Trp	Ser	Asn
Pro 65	Ala	Gln	Gln	Thr	Leu 70	Tyr	Phe	Gly	Glu	Lys 75	Arg	Ala	Leu	Arg	Asp 80
Asn	Arg	Ile	Gln	Leu 85	Val	Thr	Ser	Thr	Pro 90	His	Glu	Leu	Ser	Ile 95	Ser
Ile	Ser	Asn	Val 100	Ala	Leu	Ala	Asp	Glu 105	Gly	Glu	Tyr	Thr	Cys 110	Ser	Ile
Phe	Thr	Met 115	Pro	Val	Arg	Thr	Ala 120	Lys	Ser	Leu	Val	Thr 125	Val	Leu	Gly
Ile 130	Pro	Gln	Lys	Pro	Ile	Ile 135	Thr	Gly	Tyr	Lys	Ser 140	Ser	Leu	Arg	Glu
Lys 145	Asp	Thr	Ala	Thr	Leu 150	Asn	Cys	Gln	Ser	Ser 155	Gly	Ser	Lys	Pro	Ala 160
Ala	Arg	Leu	Thr	Trp 165	Arg	Lys	Gly	Asp	Gln 170	Glu	Leu	His	Gly	Glu 175	Pro
Thr	Arg	Ile	Gln 180	Glu	Asp	Pro	Asn	Gly 185	Lys	Thr	Phe	Thr	Val 190	Ser	Ser
Ser	Val	Thr 195	Phe	Gln	Val	Thr	Arg 200	Glu	Asp	Asp	Gly	Ala 205	Ser	Ile	Val
Cys 210	Ser	Val	Asn	His	Glu	Ser 215	Leu	Lys	Gly	Ala	Asp 220	Arg	Ser	Thr	Ser
Gln 225	Arg	Ile	Glu	Val	Leu 230	Tyr	Thr	Pro	Thr	Ala 235	Met	Ile	Arg	Pro	Asp 240
Pro	Pro	His	Pro	Arg 245	Glu	Gly	Gln	Lys	Leu 250	Leu	Leu	His	Cys	Glu 255	Gly
Arg	Gly	Asn	Pro 260	Val	Pro	Gln	Gln	Tyr 265	Leu	Trp	Glu	Lys	Glu 270	Gly	Ser
Val	Pro	Pro 275	Leu	Lys	Met	Thr	Gln 280	Glu	Ser	Ala	Leu	Ile 285	Phe	Pro	Phe

<223> Description of Artificial Sequence: Synthetic

## oligonucleotide probe

<400> 87  
 cctagcacag tgacgagggg cttggc 26

<210> 88  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 88  
 aagacacagc caccctaaac tgtcagtctt ctgggagcaa gcctgcagcc 50

<210> 89  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 89  
 gccctggcag acgagggcga gtacacctgc tcaatcttca ctatgcctgt 50

<210> 90  
 <211> 2755  
 <212> DNA  
 <213> Homo sapiens

<400> 90  
 ggggggttagg gaggaaggaa tccaccccca ccccccaaa cccttttctt ctcctttcct 60  
 ggcttcggac attggagcac taaatgaact tgaattgtgt ctgtggcgag caggatgggc 120  
 gctgttactt tgtgatgaga tcggggatga attgctcgct ttaaaaatgc tgctttggat 180  
 tctgttgctg gagacgtctc tttgttttgc cgctggaaac gttacagggg acgtttgcaa 240  
 agagaagatc tgttcctgca atgagataga aggggaccta cacgtagact gtgaaaaaaaa 300  
 gggcttcaca agtctgcagc gtttcactgc cccgacttcc cagttttacc atttatttct 360  
 gcatggcaat tccctcactc gacttttccc taatgagttc gctaactttt ataatgcggg 420  
 tagtttgcac atggaaaaca atggcttgca tgaaatcggt ccggggggctt ttctgggggct 480  
 gcagctgggtg aaaaggctgc acatcaacaa caacaagatc aagtcttttc gaaagcagac 540  
 ttttctgggg ctggacgatc tggaatatct ccaggctgat ttttaatttat tacgagatat 600  
 agaccggggg gccttcagag acttgaacaa gctggaggtg ctcattttaa atgacaatct 660  
 catcagcacc ctacctgcca acgtgttcca gtatgtgccc atcaccacc tcgacctccg 720  
 gggtaacagg ctgaaaacgc tgcctatga ggaggtcttg gagcaaatcc ctggtattgc 780  
 ggagatcctg ctagaggata acccttgagg ctgcacctgt gatctgctct ccctgaaaga 840  
 atggctggaa aacattccca agaatgccct gatcggccga gtggtctgctg aagccccac 900  
 cagactgcag ggtaaagacc tcaatgaaac caccgaacag gacttgtgtc ctttgaaaaa 960  
 ccgagtggat tctagtctcc cggcgccccc tgcccaagaa gagacctttg ctcttgagacc 1020  
 cctgccaaact cttttcaaga caaatgggca agaggatcat gccacaccag ggtctgctcc 1080

```

<210> 91
<211> 696
<212> PRT
<213> Homo sapiens

<400> 91
Met Leu Leu Trp Ile Leu Leu Leu Glu Thr Ser Leu Cys Phe Ala Ala
  1             5             10             15
Gly Asn Val Thr Gly Asp Val Cys Lys Glu Lys Ile Cys Ser Cys Asn
      20             25             30
Glu Ile Glu Gly Asp Leu His Val Asp Cys Glu Lys Lys Gly Phe Thr
      35             40             45
Ser Leu Gln Arg Phe Thr Ala Pro Thr Ser Gln Phe Tyr His Leu Phe
      50             55             60
Leu His Gly Asn Ser Leu Thr Arg Leu Phe Pro Asn Glu Phe Ala Asn
      65             70             75             80
Phe Tyr Asn Ala Val Ser Leu His Met Glu Asn Asn Gly Leu His Glu
      85             90             95

```

Ile Val Pro Gly Ala Phe Leu Gly Leu Gln Leu Val Lys Arg Leu His  
 100 105 110  
 Ile Asn Asn Asn Lys Ile Lys Ser Phe Arg Lys Gln Thr Phe Leu Gly  
 115 120 125  
 Leu Asp Asp Leu Glu Tyr Leu Gln Ala Asp Phe Asn Leu Leu Arg Asp  
 130 135 140  
 Ile Asp Pro Gly Ala Phe Gln Asp Leu Asn Lys Leu Glu Val Leu Ile  
 145 150 155 160  
 Leu Asn Asp Asn Leu Ile Ser Thr Leu Pro Ala Asn Val Phe Gln Tyr  
 165 170 175  
 Val Pro Ile Thr His Leu Asp Leu Arg Gly Asn Arg Leu Lys Thr Leu  
 180 185 190  
 Pro Tyr Glu Glu Val Leu Glu Gln Ile Pro Gly Ile Ala Glu Ile Leu  
 195 200 205  
 Leu Glu Asp Asn Pro Trp Asp Cys Thr Cys Asp Leu Leu Ser Leu Lys  
 210 215 220  
 Glu Trp Leu Glu Asn Ile Pro Lys Asn Ala Leu Ile Gly Arg Val Val  
 225 230 235 240  
 Cys Glu Ala Pro Thr Arg Leu Gln Gly Lys Asp Leu Asn Glu Thr Thr  
 245 250 255  
 Glu Gln Asp Leu Cys Pro Leu Lys Asn Arg Val Asp Ser Ser Leu Pro  
 260 265 270  
 Ala Pro Pro Ala Gln Glu Glu Thr Phe Ala Pro Gly Pro Leu Pro Thr  
 275 280 285  
 Pro Phe Lys Thr Asn Gly Gln Glu Asp His Ala Thr Pro Gly Ser Ala  
 290 295 300  
 Pro Asn Gly Gly Thr Lys Ile Pro Gly Asn Trp Gln Ile Lys Ile Arg  
 305 310 315 320  
 Pro Thr Ala Ala Ile Ala Thr Gly Ser Ser Arg Asn Lys Pro Leu Ala  
 325 330 335  
 Asn Ser Leu Pro Cys Pro Gly Gly Cys Ser Cys Asp His Ile Pro Gly  
 340 345 350  
 Ser Gly Leu Lys Met Asn Cys Asn Asn Arg Asn Val Ser Ser Leu Ala  
 355 360 365  
 Asp Leu Lys Pro Lys Leu Ser Asn Val Gln Glu Leu Phe Leu Arg Asp  
 370 375 380

09509320-071801

Asn Lys Ile His Ser Ile Arg Lys Ser His Phe Val Asp Tyr Lys Asn  
 385 390 395 400  
 Leu Ile Leu Leu Asp Leu Gly Asn Asn Asn Ile Ala Thr Val Glu Asn  
 405 410 415  
 Asn Thr Phe Lys Asn Leu Leu Asp Leu Arg Trp Leu Tyr Met Asp Ser  
 420 425 430  
 Asn Tyr Leu Asp Thr Leu Ser Arg Glu Lys Phe Ala Gly Leu Gln Asn  
 435 440 445  
 Leu Glu Tyr Leu Asn Val Glu Tyr Asn Ala Ile Gln Leu Ile Leu Pro  
 450 455 460  
 Gly Thr Phe Asn Ala Met Pro Lys Leu Arg Ile Leu Ile Leu Asn Asn  
 465 470 475 480  
 Asn Leu Leu Arg Ser Leu Pro Val Asp Val Phe Ala Gly Val Ser Leu  
 485 490 495  
 Ser Lys Leu Ser Leu His Asn Asn Tyr Phe Met Tyr Leu Pro Val Ala  
 500 505 510  
 Gly Val Leu Asp Gln Leu Thr Ser Ile Ile Gln Ile Asp Leu His Gly  
 515 520 525  
 Asn Pro Trp Glu Cys Ser Cys Thr Ile Val Pro Phe Lys Gln Trp Ala  
 530 535 540  
 Glu Arg Leu Gly Ser Glu Val Leu Met Ser Asp Leu Lys Cys Glu Thr  
 545 550 555 560  
 Pro Val Asn Phe Phe Arg Lys Asp Phe Met Leu Leu Ser Asn Asp Glu  
 565 570 575  
 Ile Cys Pro Gln Leu Tyr Ala Arg Ile Ser Pro Thr Leu Thr Ser His  
 580 585 590  
 Ser Lys Asn Ser Thr Gly Leu Ala Glu Thr Gly Thr His Ser Asn Ser  
 595 600 605  
 Tyr Leu Asp Thr Ser Arg Val Ser Ile Ser Val Leu Val Pro Gly Leu  
 610 615 620  
 Leu Leu Val Phe Val Thr Ser Ala Phe Thr Val Val Gly Met Leu Val  
 625 630 635 640  
 Phe Ile Leu Arg Asn Arg Lys Arg Ser Lys Arg Arg Asp Ala Asn Ser  
 645 650 655  
 Ser Ala Ser Glu Ile Asn Ser Leu Gln Thr Val Cys Asp Ser Ser Tyr

0909320-071801  
 0909320-071801



660

665

670

Trp His Asn Gly Pro Tyr Asn Ala Asp Gly Ala His Arg Val Tyr Asp  
 675 680 685

Cys Gly Ser His Ser Leu Ser Asp  
 690 695

&lt;210&gt; 92

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 92

gttggatctg ggcaacaata ac

22

&lt;210&gt; 93

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 93

attgttgtgc aggctgagtt taag

24

&lt;210&gt; 94

&lt;211&gt; 45

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 94

ggtggctata catggatagc aattacctgg acacgctgtc ccggg

45

&lt;210&gt; 95

&lt;211&gt; 2226

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 95

agtgcactgc gtccccctgta cccggcgcca gctgtgttcc tgaccccaga ataaactcagg 60  
 gctgcaccgg gcttggcagc gctccgcaca catttcctgt cgcggcctaa gggaaactgt 120  
 tggccgctgg gcccgcgggg ggattcttgg cagttggggg gtccgtcggg agcgagggcg 180

09509320-071801

gaggggaagg gagggggaac cgggttgggg aagccagctg tagagggcgg tgaccgcgct 240  
 ccagacacag ctctgcgtcc tcgagcggga cagatccaag ttgggagcag ctctgcgtgc 300  
 ggggcctcag agaatgagge cggcggttcgc cctgtgcctc ctctggcagg cgtcttgccc 360  
 cgggcggggc ggcggggaac accccactgc cgaccgtgct ggctgctcgg cctcgggggc 420  
 ctgctacagc ctgcaccacg ctaccatgaa gcggcaggcg gccgaggagg cctgcacctc 480  
 gcgaggtggg gcgctcagca ccgtgcgtgc gggcgccgag ctgcgcgctg tgctcgcgct 540  
 cctgcgggca ggcccagggc ccggaggggg ctccaaagac ctgctgttct gggtcgcact 600  
 ggagcgcagg cgttcccact gcacctgga gaacgagcct ttgcgggggt tctcctggct 660  
 gtctccgac cccggcggtc tcgaaagcga cagcgtgcag tgggtggagg agccccaacg 720  
 ctctgcacc gcgcggagat gcgcggtact ccaggccacc ggtgggggtc agcccgagg 780  
 ctggaaggag atgcgatgcc acctgcgcgc caacggctac ctgtgcaagt accagtttga 840  
 ggtcttgtgt cctgcgcgc gccccggggc cgctctaac ttgagctatc gcgcgccctt 900  
 ccagctgcac agcgcgcgc tggacttcag tccacctggg accgaggtga gtgcgctctg 960  
 ccggggacag ctcccgatct cagttacttg catcgcgac gaaatcggcg ctgcgtggga 1020  
 caaactctcg ggcgatgtgt tgtgtccctg cccggggagg tacctccgtg ctggcaaatg 1080  
 cgcagagctc cctaactgcc tagacgactt gggaggcttt gcctgcgaat gtgctacggg 1140  
 ctctcgagctg ggggaaggac gccgctcttg tgtgaccagt ggggaaggac agccgacct 1200  
 tggggggacc ggggtgccc ccaggcgccc gccggccact gcaaccagcc ccgtgccgca 1260  
 gagaacatgg ccaatcaggg tcgacgagaa gctgggagag acaccacttg tccctgaaca 1320  
 agacaattca gtaacatcta ttctgagat tctcgatgg ggatcacaga gcacgatgtc 1380  
 tacccttcaa atgtcccttc aagccgagtc aaaggccact atcaccccat cagggagcgt 1440  
 gatttccaag ttttaattcta cgacttctc tgccactcct caggctttcg actcctctc 1500  
 tgccgtggtc ttcatatttg tgagcacagc agtagtagtg ttggtgatct tgaccatgac 1560  
 agtactgggg cttgtcaagc tctgctttca cgaaagcccc tcttcccagc caagggaagg 1620  
 gtctatgggc ccgcccgggc tggagagtga tctgagccc gctgctttgg gctccagttc 1680  
 tgcacattgc acaacaatg ggggtgaaagt cggggactgt gatctgcggg acagagcaga 1740  
 ggggtgccttg ctggcgagg cccctcttg ctctagtgt gcatagggaa acagggggaca 1800  
 tgggcactcc tgtgaacagt ttttcacttt tgatgaaacg gggaaaccaag aggaacttac 1860  
 ttgtgtaact gacaatttct gcagaaatcc ccttctctt aaattccctt tactccactg 1920  
 aggagctaaa tcagaactgc acactccttc cctgatgata gaggaagtgg aagtgccttt 1980  
 aggatggtga tactggggga ccgggtagtg ctggggagag atattttctt atgtttattc 2040  
 ggagaatttg gagaagtgat tgaacttttc aagacattgg aaacaaatag aacacaaatat 2100  
 aatttacatt aaaaaataat ttctaccaa atggaaaggga aatgttctat gttgttcagg 2160  
 ctaggagtat attggttcga aatcccaggg aaaaaataa aaataaaaaa ttaaggatt 2220  
 gttgat 2226

<210> 96

<211> 490

<212> PRT

<213> Homo sapiens

<400> 96

Met	Arg	Pro	Ala	Phe	Ala	Leu	Cys	Leu	Leu	Trp	Gln	Ala	Leu	Trp	Pro
1				5						10				15	

Gly	Pro	Gly	Gly	Gly	Glu	His	Pro	Thr	Ala	Asp	Arg	Ala	Gly	Cys	Ser
				20					25					30	

Ala	Ser	Gly	Ala	Cys	Tyr	Ser	Leu	His	His	Ala	Thr	Met	Lys	Arg	Gln
			35					40					45		

Ala	Ala	Glu	Glu	Ala	Cys	Ile	Leu	Arg	Gly	Gly	Ala	Leu	Ser	Thr	Val
		50					55				60				

Arg Ala Gly Ala Glu Leu Arg Ala Val Leu Ala Leu Leu Arg Ala Gly  
 65 70 75 80  
 Pro Gly Pro Gly Gly Gly Ser Lys Asp Leu Leu Phe Trp Val Ala Leu  
 85 90 95  
 Glu Arg Arg Arg Ser His Cys Thr Leu Glu Asn Glu Pro Leu Arg Gly  
 100 105 110  
 Phe Ser Trp Leu Ser Ser Asp Pro Gly Gly Leu Glu Ser Asp Thr Leu  
 115 120 125  
 Gln Trp Val Glu Glu Pro Gln Arg Ser Cys Thr Ala Arg Arg Cys Ala  
 130 135 140  
 Val Leu Gln Ala Thr Gly Gly Val Glu Pro Ala Gly Trp Lys Glu Met  
 145 150 155 160  
 Arg Cys His Leu Arg Ala Asn Gly Tyr Leu Cys Lys Tyr Gln Phe Glu  
 165 170 175  
 Val Leu Cys Pro Ala Pro Arg Pro Gly Ala Ala Ser Asn Leu Ser Tyr  
 180 185 190  
 Arg Ala Pro Phe Gln Leu His Ser Ala Ala Leu Asp Phe Ser Pro Pro  
 195 200 205  
 Gly Thr Glu Val Ser Ala Leu Cys Arg Gly Gln Leu Pro Ile Ser Val  
 210 215 220  
 Thr Cys Ile Ala Asp Glu Ile Gly Ala Arg Trp Asp Lys Leu Ser Gly  
 225 230 235 240  
 Asp Val Leu Cys Pro Cys Pro Gly Arg Tyr Leu Arg Ala Gly Lys Cys  
 245 250 255  
 Ala Glu Leu Pro Asn Cys Leu Asp Asp Leu Gly Gly Phe Ala Cys Glu  
 260 265 270  
 Cys Ala Thr Gly Phe Glu Leu Gly Lys Asp Gly Arg Ser Cys Val Thr  
 275 280 285  
 Ser Gly Glu Gly Gln Pro Thr Leu Gly Gly Thr Gly Val Pro Thr Arg  
 290 295 300  
 Arg Pro Pro Ala Thr Ala Thr Ser Pro Val Pro Gln Arg Thr Trp Pro  
 305 310 315 320  
 Ile Arg Val Asp Glu Lys Leu Gly Glu Thr Pro Leu Val Pro Glu Gln  
 325 330 335  
 Asp Asn Ser Val Thr Ser Ile Pro Glu Ile Pro Arg Trp Gly Ser Gln

09909320 071801  
 02E60660

340                      345                      350  
 Ser Thr Met Ser Thr Leu Gln Met Ser Leu Gln Ala Glu Ser Lys Ala  
                     355                      360                      365  
 Thr Ile Thr Pro Ser Gly Ser Val Ile Ser Lys Phe Asn Ser Thr Thr  
                     370                      375                      380  
 Ser Ser Ala Thr Pro Gln Ala Phe Asp Ser Ser Ser Ala Val Val Phe  
 385                      390                      395                      400  
 Ile Phe Val Ser Thr Ala Val Val Val Leu Val Ile Leu Thr Met Thr  
                     405                      410                      415  
 Val Leu Gly Leu Val Lys Leu Cys Phe His Glu Ser Pro Ser Ser Gln  
                     420                      425                      430  
 Pro Arg Lys Glu Ser Met Gly Pro Pro Gly Leu Glu Ser Asp Pro Glu  
                     435                      440                      445  
 Pro Ala Ala Leu Gly Ser Ser Ser Ala His Cys Thr Asn Asn Gly Val  
                     450                      455                      460  
 Lys Val Gly Asp Cys Asp Leu Arg Asp Arg Ala Glu Gly Ala Leu Leu  
 465                      470                      475                      480  
 Ala Glu Ser Pro Leu Gly Ser Ser Asp Ala  
                     485                      490

&lt;210&gt; 97

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 97

tggaaggaga tgcgatgccca cctg

24

&lt;210&gt; 98

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 98

tgaccagtgg ggaaggacag

20

FOBT40-02E60660

```
<210> 99
<211> 20
<212> DNA
<213> Artificial Sequence
```

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

```
<400> 99
acagagcaga ggggtgccttg                20
```

```
<210> 100
<211> 24
<212> DNA
<213> Artificial Sequence
```

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 100  
tcagggacaa gtggtgtctc tccc 24

```
<210> 101
<211> 24
<212> DNA
<213> Artificial Sequence
```

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 101  
tcaggggaagg agtgtgcagt tctg 24

```
<210> 102
<211> 50
<212> DNA
<213> Artificial Sequence
```

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 102  
acagctcccg atctcagtta cttgcatcgc ggacgaaatc ggcgcctcgc 50

```
<210> 103
<211> 2026
<212> DNA
<213> Homo sapiens
```

&lt;400&gt; 103

```

cggacgcgtg ggattcagca gtggcctgtg gctgccagag cagctcctca ggggaaacta 60
agcgtcgagt cagacggcac cataatcgcc tttaaaagtg cctccgccct gccggccgcg 120
tatcccccg cttacctgggc cgccccgcgg cggtgcgcgc gtgagaggga gcgcgcgggc 180
agccgagcgc cgggtgtgagc cagcgtgtgt gccagtgtga gcggcggtgt gaggcgcgtg 240
ggtgcggagg ggctgtgtgt ccggcgcgcg cgccgtgggg tgcaaaccac gaggctctac 300
gctgccatga ggggcgcgaa cgccctgggc ccactctgcc tgctgctggc tgccgccacc 360
cagctctcgc ggcagcagtc cccagagaga cctgttttca catgtggtgg cattcttact 420
ggagagtctg gatttattgg cagtgaaggt tttcctggag tgtaccctcc aaatagcaaa 480
tgtacttgga aaatcacagt tcccgaagga aaagtagtcg ttctcaattt ccgattcata 540
gacctcgaga gtgacaacct gtgccgctat gactttgtgg atgtgtacaa tggccatgcc 600
aatggccagc gcattggccg cttctgtggc actttccggc ctggagccct tgtgtccagt 660
ggcaacaaga tgatggtgca gatgatttct gatgccaaca cagctggcaa tggcttcatg 720
gccatgttct ccgtgctga accaaacgaa agaggggatc agtattgtgg aggactcctt 780
gacagacctt ccggctcttt taaaaccccc aactggccag accgggatta ccctgcagga 840
gtcacttggt tgtggcacat ttagaccca aagaatcagc ttatagaatt aaagtttgag 900
aagtttgatg tggagcgaga taactactgc cgatatgatt atgtggctgt gtttaatggc 960
ggggaagtca acgatgctag aagaattgga aagtattgtg gtgatagtcc acctgcgcca 1020
attgtgtctg agagaaatga acttcttatt cagtttttat cagacttaag tttactgca 1080
gatgggttta ttggctacta catattcagg ccaaaaaaac tgctacaac tacagaacag 1140
cctgtcacca ccacattccc tgtaaccacg gggttaaaac ccaccgtggc cttgtgtcaa 1200
caaaagtgtg gacggacggg gactctggag ggcaattatt gttcaagtga ctttgtatta 1260
gccggcactg ttatcacaa cactactcgc gatgggagtt tgcacgccac agtctcgatc 1320
atcaacatct acaaagaggg aaatttggcg attcagcagg cgggcaagaa catgagtgcc 1380
aggctgactg tcgtctgcaa gcagtgccct ctctcagaa gaggtctaaa ttacattatt 1440
atgggccaag taggtgaaga tgggcgaggg aaaaatcatgc caaacagctt tatcatgatg 1500
ttcaagacca agaatcagaa gctcctggat gccttaaaaa ataagcaatg ttaacagtga 1560
actgtgtcca ttaagctgt attctgccat tgcttttgaa agatctatgt tctctcagta 1620
gaaaaaaaa tacttataaa attacatatt ctgaaagagg attccgaaag atgggactgg 1680
ttgactcttc acatgatgga ggtatgaggg ctccgagata gctgagggaa gttctttgcc 1740
tgctgtcaga ggagcagcta tctgattgga aacctgccga cttagtgcgg tgataggaag 1800
ctaaaagtgt caagcgttga cagcttggaa gcgtttattt atacatctct gtaaaaggat 1860
attttagaat tgagttgtgt gaagatgtca aaaaaagatt ttagaagtgc aatatttata 1920
gtgttatttg tttcaccttc aagcctttgc cctgaggtgt tacaatcttg tcttgcgttt 1980
tctaaatcaa tgcttaataa aatattttta aaggaaaaaa aaaaaa 2026

```

&lt;210&gt; 104

&lt;211&gt; 415

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 104

```

Met Arg Gly Ala Asn Ala Trp Ala Pro Leu Cys Leu Leu Leu Ala Ala
  1             5             10             15

```

```

Ala Thr Gln Leu Ser Arg Gln Gln Ser Pro Glu Arg Pro Val Phe Thr
      20             25             30

```

```

Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly Ser Glu Gly
      35             40             45

```

```

Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr
      50             55             60

```

Val Pro Glu Gly Lys Val Val Val Leu Asn Phe Arg Phe Ile Asp Leu  
 65 70 75 80  
 Glu Ser Asp Asn Leu Cys Arg Tyr Asp Phe Val Asp Val Tyr Asn Gly  
 85 90 95  
 His Ala Asn Gly Gln Arg Ile Gly Arg Phe Cys Gly Thr Phe Arg Pro  
 100 105 110  
 Gly Ala Leu Val Ser Ser Gly Asn Lys Met Met Val Gln Met Ile Ser  
 115 120 125  
 Asp Ala Asn Thr Ala Gly Asn Gly Phe Met Ala Met Phe Ser Ala Ala  
 130 135 140  
 Glu Pro Asn Glu Arg Gly Asp Gln Tyr Cys Gly Gly Leu Leu Asp Arg  
 145 150 155 160  
 Pro Ser Gly Ser Phe Lys Thr Pro Asn Trp Pro Asp Arg Asp Tyr Pro  
 165 170 175  
 Ala Gly Val Thr Cys Val Trp His Ile Val Ala Pro Lys Asn Gln Leu  
 180 185 190  
 Ile Glu Leu Lys Phe Glu Lys Phe Asp Val Glu Arg Asp Asn Tyr Cys  
 195 200 205  
 Arg Tyr Asp Tyr Val Ala Val Phe Asn Gly Gly Glu Val Asn Asp Ala  
 210 215 220  
 Arg Arg Ile Gly Lys Tyr Cys Gly Asp Ser Pro Pro Ala Pro Ile Val  
 225 230 235 240  
 Ser Glu Arg Asn Glu Leu Leu Ile Gln Phe Leu Ser Asp Leu Ser Leu  
 245 250 255  
 Thr Ala Asp Gly Phe Ile Gly His Tyr Ile Phe Arg Pro Lys Lys Leu  
 260 265 270  
 Pro Thr Thr Thr Glu Gln Pro Val Thr Thr Thr Phe Pro Val Thr Thr  
 275 280 285  
 Gly Leu Lys Pro Thr Val Ala Leu Cys Gln Gln Lys Cys Arg Arg Thr  
 290 295 300  
 Gly Thr Leu Glu Gly Asn Tyr Cys Ser Ser Asp Phe Val Leu Ala Gly  
 305 310 315 320  
 Thr Val Ile Thr Thr Ile Thr Arg Asp Gly Ser Leu His Ala Thr Val  
 325 330 335  
 Ser Ile Ile Asn Ile Tyr Lys Glu Gly Asn Leu Ala Ile Gln Gln Ala

0909330-071301  
 0909330-071301

340	345	350
Gly Lys Asn Met Ser Ala Arg Leu Thr Val Val Cys Lys Gln Cys Pro		
355	360	365
Leu Leu Arg Arg Gly Leu Asn Tyr Ile Ile Met Gly Gln Val Gly Glu		
370	375	380
Asp Gly Arg Gly Lys Ile Met Pro Asn Ser Phe Ile Met Met Phe Lys		
385	390	400
Thr Lys Asn Gln Lys Leu Leu Asp Ala Leu Lys Asn Lys Gln Cys		
405	410	415

&lt;210&gt; 105

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 105

ccgattcata gacctcgaga gt

22

&lt;210&gt; 106

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 106

gtcaaggagt cctccacaat ac

22

&lt;210&gt; 107

&lt;211&gt; 45

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 107

gtgtacaatg gccatgccaa tggccagcgc attggccgct tctgt

45

&lt;210&gt; 108

&lt;211&gt; 1838

&lt;212&gt; DNA

T03F20"02E6060



<213> Homo sapiens

<400> 108

```

cggacgcgtg ggcggacgcg tgggcggccc acggcgcccc cgggctgggg cggtcgcttc 60
ttcctttctc gtggcctacg aggggtcccca gcctgggtaa agatggcccc atggcccccg 120
aagggcctag tcccagctgt gctctggggc ctcagcctct tctcaacct cccaggacct 180
atctggctcc agccctctcc acctccccag tcttctcccc cgctcagcc ccatccgtgt 240
catacctgcc ggggactggt tgacagcttt aacaagggcc tggagagaac catccgggac 300
aactttggag gtggaaacac tgcctgggag gaagagaatt tgtccaaata caaagacagt 360
gagacccgcc tggtagaggt gctggagggt gtgtgcagca agtcagactt cgagtgccac 420
cgctgctgg agctgagtga ggagctgggt gagagctgggt ggtttcacaa gcagcaggag 480
gccccggacc tcttccagtg gctgtgctca gattccctga agctctgtg ccccgaggc 540
accttcgggc cctcctgct tccctgtcct gggggaacag agaggccctg cggtggtctac 600
gggcagtgtg aaggagaagg gacacgaggg ggcagcgggc actgtgactg ccaagccggc 660
tacgggggtg aggcctgtgg ccagtgtggc cttggctact ttgaggcaga acgcaacgcc 720
agccatctgg tatgttcggc ttgttttggc cctgtgccc gatgctcagg acctgaggaa 780
tcaaactggt tgcaatgcaa gaagggtggt gccctgcatc acctcaagtg tgtagacatt 840
gatgagtgtg gcacagaggg agccaactgt ggagctgacc aattctgctg gaacactgag 900
ggctcctatg agtgccgaga ctgtgccaag gcctgcctag gctgcatggg ggcagggcca 960
ggtcgctgta agaagtgtag ccctggctat cagcaggtgg gctccaagtg tctcgatgtg 1020
gatgagtgtg agacagaggt gtgtccggga gagaacaagc agtgtgaaaa caccgagggc 1080
ggttatcgct gcatctgtgc cgagggtctac aagcagatgg aaggcatctg tgtgaaggag 1140
cagatcccag agtcagcagg cttcttctca gagatgacag aagacgagtt ggtggtgctg 1200
cagcagatgt tctttggcat catcatctgt gcaactggcca cgctggctgc taaggggcag 1260
ttggtgttca ccgccatctt cattggggct gtggcgggcca tgactggcta ctggttgtca 1320
gagcgctagt accgtgtgct ggagggttc atcaagggca gataatcgcg gccaccacct 1380
gtaggacctc ctcccaccca cgctgcccc agagcttggtg ctgcccctct gctggacact 1440
caggacagct tggtttat ttgagagtgg ggtaagcacc cctacctgcc ttacagagca 1500
gcccaggtac ccaggcccgg gcagacaagg cccctgggggt aaaaagtagc cctgaagggtg 1560
gataccatga gctcttcacc tggcggggac tggcaggctt cacaatgtgt gaatttcaaa 1620
agtttttct taatgggtgg tgctagagct ttggcccctg cttaggatta ggtggtcctc 1680
acaggggtgg ggccatcaca gctccctcct gccagctgca tgctgccagt tcctgttctg 1740
tgttcaccac atccccacac cccattgcc aattattatt catctcagga aataaagaaa 1800
ggtcttgtaa agttaaaaaa aaaaaaaaaa aaaaaaaa 1838

```

<210> 109

<211> 420

<212> PRT

<213> Homo sapiens

<400> 109

```

Met Ala Pro Trp Pro Pro Lys Gly Leu Val Pro Ala Val Leu Trp Gly
  1                      5                      10                      15

Leu Ser Leu Phe Leu Asn Leu Pro Gly Pro Ile Trp Leu Gln Pro Ser
      /                      20                      25                      30

Pro Pro Pro Gln Ser Ser Pro Pro Pro Gln Pro His Pro Cys His Thr
      35                      40                      45

Cys Arg Gly Leu Val Asp Ser Phe Asn Lys Gly Leu Glu Arg Thr Ile
      50                      55                      60

```

0909320.071301

Arg Asp Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Glu Asn Leu  
 65 70 75 80  
 Ser Lys Tyr Lys Asp Ser Glu Thr Arg Leu Val Glu Val Leu Glu Gly  
 85 90 95  
 Val Cys Ser Lys Ser Asp Phe Glu Cys His Arg Leu Leu Glu Leu Ser  
 100 105 110  
 Glu Glu Leu Val Glu Ser Trp Trp Phe His Lys Gln Gln Glu Ala Pro  
 115 120 125  
 Asp Leu Phe Gln Trp Leu Cys Ser Asp Ser Leu Lys Leu Cys Cys Pro  
 130 135 140  
 Ala Gly Thr Phe Gly Pro Ser Cys Leu Pro Cys Pro Gly Gly Thr Glu  
 145 150 155 160  
 Arg Pro Cys Gly Gly Tyr Gly Gln Cys Glu Gly Glu Gly Thr Arg Gly  
 165 170 175  
 Gly Ser Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Gly Glu Ala Cys  
 180 185 190  
 Gly Gln Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ala Ser His  
 195 200 205  
 Leu Val Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Ser Gly Pro  
 210 215 220  
 Glu Glu Ser Asn Cys Leu Gln Cys Lys Lys Gly Trp Ala Leu His His  
 225 230 235 240  
 Leu Lys Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gly Ala Asn Cys  
 245 250 255  
 Gly Ala Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg  
 260 265 270  
 Asp Cys Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Arg  
 275 280 285  
 Cys Lys Lys Cys Ser Pro Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu  
 290 295 300  
 Asp Val Asp Glu Cys Glu Thr Glu Val Cys Pro Gly Glu Asn Lys Gln  
 305 310 315 320  
 Cys Glu Asn Thr Glu Gly Gly Tyr Arg Cys Ile Cys Ala Glu Gly Tyr  
 325 330 335  
 Lys Gln Met Glu Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala  
 340 345 350

09909320-071801

Gly Phe Phe Ser Glu Met Thr Glu Asp Glu Leu Val Val Leu Gln Gln  
 355 360 365

Met Phe Phe Gly Ile Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys  
 370 375 380

Gly Asp Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met  
 385 390 395 400

Thr Gly Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe  
 405 410 415

Ile Lys Gly Arg  
 420

<210> 110

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 110

cctggctatc agcaggtggg ctccaagtgt ctcgatgtgg atgagtgtga 50

<210> 111

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 111

attctgcgtg aacactgagg gc 22

<210> 112

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 112

atctgcttgt agccctcggc ac 22

<210> 113

FOR "0" CEE60660

<211> 1616  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (1461)  
 <223> a, t, c or g

<400> 113  
 tgagaccctc ctgcagcctt ctcaagggac agccccactc tgccctcttgc tcctccaggg 60  
 cagcaccatg cagccctgt ggcctctgctg ggcactcttg gtgttgcccc tggccagccc 120  
 cggggccgcc ctgaccgggg agcagctcct gggcagcctg ctgcggcagc tgcagctcaa 180  
 agaggtgccc accctggaca gggccgacat ggaggagctg gtcaccccc cccacgtgag 240  
 ggcccagtac gtggccctgc tgcagcgcag ccacggggac cgctcccgcg gaaagaggtt 300  
 cagccagagc ttccgagagg tggccggcag gttcctggcg ttggaggcca gcacacacct 360  
 gctggtgttc ggcattggagc agcggctgcc gcccaacagc gagctggtgc aggcctgtgt 420  
 gcggtctctc caggagccgg tccccaaagg cgcgctgcac aggcacgggc ggctgtcccc 480  
 gcgcagcgcc cggggccggg tgaccgtcga gtggctgcgc gtccgcgacg acggctccaa 540  
 ccgcacctcc ctcatcgact ccaggtctgt gtccgtccac gagagcggct ggaaggcctt 600  
 cgacgtgacc gaggcctga acttctggca gcagctgagc cgcccccgcc agcctgtgt 660  
 gctacaggtg tcggtgcaga gggagcatct gggcccgctg gcgtccggcg cccacaagct 720  
 ggtccgcttt gcctcgcagg gggcgccagc cgggcttggt gagccccagc tggagctgca 780  
 caccctggac cttggggact atggagctca gggcgactgt gaccctgaag caccaatgac 840  
 cgagggcacc cgctgctgcc gccaggagat gtacattgac ctgcagggga tgaagtgggc 900  
 cgagaactgg gtgctggagc ccccgggctt cctggcttat gagtgtgtgg gcacctgccg 960  
 gcagcccccg gaggccttgg ccttcaagtg gccgtttctg gggcctcgac agtgcacgc 1020  
 ctcgagact gactcgtgc ccatgatcgt cagcatcaag gagggaggca ggaccaggcc 1080  
 ccaggtggtc agcctgccc acatgagggt gcagaagtgc agctgtgcct cggatggtgc 1140  
 gctcgtgcca aggaggctcc agccataggc gcctagtgtg gccatcgagg gacttgactt 1200  
 gtgtgtgttt ctgaagtgtt cgagggtacc aggagagctg gcgatgactg aactgctgat 1260  
 ggacaaatgc tctgtgtct ctagttagcc ctgaatttgc ttctctgac aagttaacct 1320  
 acctaatatt tgcttctcag gaatgagaat ctttggccac tggagagccc ttgctcagtt 1380  
 ttctctattt ttattattca ctgcactata ttctaagcac ttacatgtgg agatactgta 1440  
 acctgagggc agaaagccca ntgtgtcatt gtttacttgt cctgtcactg gatctgggct 1500  
 aaagtccctc accaccactc tggacctaa acctgggggt aagtgtgggt tgtgcatccc 1560  
 caatccagat aataaagact ttgtaaaaca tgaataaaac acattttatt ctaaaa 1616

<210> 114  
 <211> 366  
 <212> PRT  
 <213> Homo sapiens

<400> 114  
 Met Gln Pro Leu Trp Leu Cys Trp Ala Leu Trp Val Leu Pro Leu Ala  
 1 5 10 15  
 Ser Pro Gly Ala Ala Leu Thr Gly Glu Gln Leu Leu Gly Ser Leu Leu  
 20 25 30  
 Arg Gln Leu Gln Leu Lys Glu Val Pro Thr Leu Asp Arg Ala Asp Met  
 35 40 45

09909320.071801

Glu Glu Leu Val Ile Pro Thr His Val Arg Ala Gln Tyr Val Ala Leu  
 50 55 60  
 Leu Gln Arg Ser His Gly Asp Arg Ser Arg Gly Lys Arg Phe Ser Gln  
 65 70 75 80  
 Ser Phe Arg Glu Val Ala Gly Arg Phe Leu Ala Leu Glu Ala Ser Thr  
 85 90 95  
 His Leu Leu Val Phe Gly Met Glu Gln Arg Leu Pro Pro Asn Ser Glu  
 100 105 110  
 Leu Val Gln Ala Val Leu Arg Leu Phe Gln Glu Pro Val Pro Lys Ala  
 115 120 125  
 Ala Leu His Arg His Gly Arg Leu Ser Pro Arg Ser Ala Arg Ala Arg  
 130 135 140  
 Val Thr Val Glu Trp Leu Arg Val Arg Asp Asp Gly Ser Asn Arg Thr  
 145 150 155 160  
 Ser Leu Ile Asp Ser Arg Leu Val Ser Val His Glu Ser Gly Trp Lys  
 165 170 175  
 Ala Phe Asp Val Thr Glu Ala Val Asn Phe Trp Gln Gln Leu Ser Arg  
 180 185 190  
 Pro Arg Gln Pro Leu Leu Leu Gln Val Ser Val Gln Arg Glu His Leu  
 195 200 205  
 Gly Pro Leu Ala Ser Gly Ala His Lys Leu Val Arg Phe Ala Ser Gln  
 210 215 220  
 Gly Ala Pro Ala Gly Leu Gly Glu Pro Gln Leu Glu Leu His Thr Leu  
 225 230 235 240  
 Asp Leu Gly Asp Tyr Gly Ala Gln Gly Asp Cys Asp Pro Glu Ala Pro  
 245 250 255  
 Met Thr Glu Gly Thr Arg Cys Cys Arg Gln Glu Met Tyr Ile Asp Leu  
 260 265 270  
 Gln Gly Met Lys Trp Ala Glu Asn Trp Val Leu Glu Pro Pro Gly Phe  
 275 280 285  
 Leu Ala Tyr Glu Cys Val Gly Thr Cys Arg Gln Pro Pro Glu Ala Leu  
 290 295 300  
 Ala Phe Lys Trp Pro Phe Leu Gly Pro Arg Gln Cys Ile Ala Ser Glu  
 305 310 315 320  
 Thr Asp Ser Leu Pro Met Ile Val Ser Ile Lys Glu Gly Gly Arg Thr  
 325 330 335

09909320-071801

Arg Pro Gln Val Val Ser Leu Pro Asn Met Arg Val Gln Lys Cys Ser  
 340 345 350

Cys Ala Ser Asp Gly Ala Leu Val Pro Arg Arg Leu Gln Pro  
 355 360 365

<210> 115

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 115

aggactgccca taacttgccct g

21

<210> 116

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 116

ataggagttg aagcagcgct gc

22

<210> 117

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 117

tgtgtggaca tagacgagtg ccgctaccgc tactgccagc accgc

45

<210> 118

<211> 1857

<212> DNA

<213> Homo sapiens

<400> 118

gtctgttccc aggagtcctt cggcggctgt tgtgtcagtg gcctgatcgc gatggggaca 60  
 aaggcgcaag tcgagaggaa actgttgctgc ctcttcatat tggcgatcct gttgtgctcc 120  
 ctggcattgg gcagtgttac agtgcaactct tctgaacctg aagtcagaat tcctgagaat 180

09909330-071801

aatcctgtga agttgtcctg tgcctactcg ggctttttctt ctccccgtgt ggagtgggaag 240  
 tttgaccaag gagacaccac cagactcggt tgctataata acaagatcac agcttcctat 300  
 gaggaccggg tgaccttctt gccaaactggt atcaccttca agtccgtgac acgggaagac 360  
 actgggacat acacttgtat ggtctctgag gaaggcggca acagctatgg ggaggtcaag 420  
 gtcaagctca tcgtgcttgt gcctccatcc aagcctacag ttaacatccc ctctctgcc 480  
 accattggga accgggcagt gctgacatgc tcagaacaag atgggtcccc acctctgaa 540  
 tacacctggt tcaaagatgg gatagtgat cctacgaatc ccaaaagcac ccgtgccttc 600  
 agcaactctt cctatgtcct gaatcccaca acaggagagc tgggtcttga tccccgtca 660  
 gcctctgata ctggagaata cagctgtgag gcacgggaatg ggtatgggac acccatgact 720  
 tcaaagtctg tgcgcatgga agctgtggag cggaaatgtg gggatcatcg ggcagccgtc 780  
 cttgtaaccc tgattctcct gggaatcttg gtttttggca tctgggttgc ctatagccga 840  
 ggccactttg acagaacaaa gaaagggaact tcgagtaaga aggtgattta cagccagcct 900  
 agtgcctgaa gtgaaggaga attcaaacag acctcgatcat tcctggtgtg agcctggtcg 960  
 gctcaccgcc tatcatctgc atttgcttca ctcagggtgct accggactct ggccccctgat 1020  
 gtctgtagtt tcacaggatg ccttatttgt cttctacacc ccacagggcc cctacttct 1080  
 tcggatgtgt ttttaataat gtcagctatg tgccccatcc tccttcatgc cctccctccc 1140  
 tttcctacca ctgctgagtg gcctggaact tgtttaaagt gtttattccc catttctttg 1200  
 agggatcagg aaggaatcct gggatgcca ttgacttccc ttctaagtag acagcaaaaa 1260  
 tggcgggggt cgcaggaatc tgcactcaac tgcccacctg gctggcaggg atctttgaat 1320  
 aggtatcttg agcttgggtc tgggctcttt ccttgtgtac tgacgaccag ggccagctgt 1380  
 tctagagcgg gaattagagg ctagagcggc tgaaatggtt gtttgggtgat gacactgggg 1440  
 tccttccatc tctggggccc actctcttct gtcttcccat gggaaagtgc actgggatcc 1500  
 ctctgccccg tcctcctgaa tacaagctga ctgacattga ctgtgtctgt ggaaaatggg 1560  
 agctcttgtt gtggagagca tagtaaattt tcagagaact tgaagccaaa aggattttaa 1620  
 accgctgctc taaagaaaag aaaactggag gctgggcgca gtggctcacg cctgtaatcc 1680  
 cagaggctga ggcaggcgga tcacctgagg tcgggagttc gggatcagcc tgaccaacat 1740  
 ggagaaaccc tactggaaat acaaagttag ccaggcatgg tggtgcatgc ctgtagtccc 1800  
 agctgctcag gagcctggca acaagagcaa aactccagct caaaaaaaaa aaaaaaa 1857

<210> 119

<211> 299

<212> PRT

<213> Homo sapiens

<400> 119

Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile  
 1 5 10 15  
 Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His  
 20 25 30  
 Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu  
 35 40 45  
 Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe  
 50 55 60  
 Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr  
 65 70 75 80  
 Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe  
 85 90 95

```
<210> 120
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
        oligonucleotide probe

<400> 120
tcgcggagct gtgttctgtt tccc

<210> 121
<211> 50
```



<212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 121  
 tgatcgcgat ggggacaaag gcgcaagctc gagaggaaac tgttgtgcct 50  
  
 <210> 122  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 122  
 acacctggtt caaagatggg 20  
  
 <210> 123  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 123  
 taggaagagt tgctgaaggc acgg 24  
  
 <210> 124  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 124  
 ttgccttact caggtgctac 20  
  
 <210> 125  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic

0909320-01301  
 T03T20 02E60650

## oligonucleotide probe

<400> 125  
actcagcagt ggtaggaaag 20

<210> 126  
<211> 1210  
<212> DNA  
<213> Homo sapiens

<400> 126  
cagcgcgtgg ccggcgccgc tgtgggggaca gcatgagcgg cggttggatg gcgcagggttg 60  
gagcgtggcg aacaggggct ctgggcctgg cgctgctgct gctgctcggc ctcggactag 120  
gcctggaggc cgccgcgagc ccgctttcca ccccgacctc tgcccaggcc gcaggcccca 180  
gctcaggctc gtgcccaccc accaagttcc agtgccgcac cagtggctta tgcgtgcccc 240  
tcacctggcg ctgcgacagg gacttggact gcagcgatgg cagcgatgag gaggagtgc 300  
ggattgagcc atgtacccag aaagggcaat gcccaccgcc ccttggcctc ccttggccct 360  
gcaccggcgt cagtgactgc tctgggggaa ctgacaagaa actgcgcaac tgcagccgcc 420  
tggcctgcct agcaggcgag ctccgttgca cgctgagcga tgactgcatt ccactcacgt 480  
ggcgctgcga cggccaccca gactgtcccg actccagcga cgagctcggc tgtggaacca 540  
atgagatcct cccggaaggg gatgccacaa ccatggggcc ccttgtgacc ctggagagtg 600  
tcacctctct caggaatgcc acaaccatgg ggccccctgt gaccctggag agtgtcccct 660  
ctgtcgggaa tgccacatcc tcctctgccg gagaccagtc tggaaagcca actgcctatg 720  
gggttattgc agctgctgcg gtgctcagtg caagcctggc caccgccacc ctctccttt 780  
tgtcctggct ccgagcccag gagcgccctc gccactggg gttactgggt gccatgaagg 840  
agtccctgct gctgtcagaa cagaagacct cgctgccctg aggacaagca cttgccacca 900  
ccgtcactca gccctgggcg tagccggaca ggaggagagc agtgatgcgg atgggtaccc 960  
gggcacacca gccctcagag acctgagttc ttctggccac gtggaacctc gaaccggagc 1020  
tcctgcagaa gtggccctgg agattgaggg tccttgagca ctccctatgg agatccgggg 1080  
agctaggatg gggaacctgc cacagccaga actgaggggc tggccccagg cagctcccag 1140  
ggggtagaac ggccctgtgc ttaagacact ccttgcctgc ccgtctgagg gtggcgatta 1200  
aagttgcttc 1210

<210> 127  
<211> 282  
<212> PRT  
<213> Homo sapiens

<400> 127  
Met Ser Gly Gly Trp Met Ala Gln Val Gly Ala Trp Arg Thr Gly Ala  
1 5 10 15  
Leu Gly Leu Ala Leu Leu Leu Leu Leu Gly Leu Gly Leu Gly Leu Glu  
20 25 30  
Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly  
35 40 45  
Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser  
50 55 60  
Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys  
65 70 75 80

0909330.071301

24

<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 129  
 ttggttccac agccgagctc gtcg 24

<210> 130  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 130  
 gaggaggagt gcaggattga gccatgtacc cagaaagggc aatgcccacc 50

<210> 131  
 <211> 1843  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (1837)  
 <223> a, t, c or g

<400> 131  
 cccacgcgtc cgggtctcgt cgtctgcgca gcggcgccag cagagggtcgc gcacagatgc 60  
 ggggttagact ggccggggga ggaggcggag gagggaagga agctgcatgc atgagacca 120  
 cagactcttg caagctggat gccctctgtg gatgaaagat gtatcatgga atgaaccga 180  
 gcaatggaga tggatttcta gagcagcagc agcagcagca gcaacctcag tccccccaga 240  
 gactcttggc cgtgatcctg tggtttcagc tggcgctgtg ctccggccct gcacagctca 300  
 cgggcggggt cgatgacctt caagtgtgtg ctgaccccg gattcccgag aatggcttca 360  
 ggacccccag cggagggggt ttctttgaag gctctgtagc ccgatttcac tgccaagacg 420  
 gattcaagct gaagggcgct acaaagagac tgtgtttgaa gcattttaat ggaaccctag 480  
 gctggatccc aagtgataat tccatctgtg tgcaagaaga ttgccgtatc cctcaaatcg 540  
 aagatgctga gattcataac aagacatata gacatggaga gaagctaata atcacttgtc 600  
 atgaaggatt caagatccgg taccocgacc tacacaatat ggtttcatta tgcgcgatg 660  
 atggaacgtg gaataatctg cccatctgtc aaggctgcct gagacctcta gcctcttcta 720  
 atggctatgt aaacatctct gagctccaga cctccttccc ggtggggact gtgatctcct 780  
 atcgtctgctt tcccggattt aaacttgatg ggtctgcgta tcttgagtgc ttacaaaacc 840  
 ttatctggtc gtccagccca ccccggtgcc ttgctctgga agcccaagtc tgtccactac 900  
 ctccaatggt gagtcacgga gatttcgtct gccaccccg gccttgtagc cgctacaacc 960  
 acggaactgt ggtggagttt tactgcgatc ctggctacag cctcaccagc gactacaagt 1020  
 acatcacctg ccagtatgga gagtggtttc cttcttatca agtctactgc atcaaatcag 1080  
 agcaaactg gccagcacc catgagaccc tctgaccac gtggaagatt gtggcggttca 1140

```

cggcaaccag tgtgctgctg gtgctgctgc tcgtcatcct ggccaggatg ttccagacca 1200
agttcaaggc ccactttccc cccagggggc ctccccggag ttccagcagt gacctgact 1260
ttgtggtggt agacggcgtg cccgtcatgc tcccgtccta tgacgaagct gtgagtggcg 1320
gcttgagtgc cttaggcccc gggtagatgg cctctgtggg ccagggtgc cccttaccg 1380
tggacgacca gagcccccca gcataccccg gctcagggga cacggacaca ggcccagggg 1440
agtcagaaac ctgtgacagc gtctcaggct cttctgagct gctccaaagt ctgtattcac 1500
ctcccagggtg ccaagagagc acccaccctg cttcgggaaa ccctgacata attgccagca 1560
cggcagagga ggtggcatcc accagcccag gcatccatca tgcccactgg gtgttggtcc 1620
taagaaactg attgattaaa aaatttccca aagtgtcctg aagtgtctct tcaaatacat 1680
gttgatctgt ggagttgatt cctttccttc tcttggtttt agacaaatgt aaacaaagct 1740
ctgatactta aaattgctat gctgatagag tggtaggggc tggaagcttg atcaagtcct 1800
gtttcttctt gacacagact gattaaaaat taaaagnaaa aaa 1843

```

<210> 132

<211> 490

<212> PRT

<213> Homo sapiens

<400> 132

```

Met Tyr His Gly Met Asn Pro Ser Asn Gly Asp Gly Phe Leu Glu Gln
  1             5             10             15

```

```

Gln Gln Gln Gln Gln Gln Pro Gln Ser Pro Gln Arg Leu Leu Ala Val
      20             25             30

```

```

Ile Leu Trp Phe Gln Leu Ala Leu Cys Phe Gly Pro Ala Gln Leu Thr
      35             40             45

```

```

Gly Gly Phe Asp Asp Leu Gln Val Cys Ala Asp Pro Gly Ile Pro Glu
      50             55             60

```

```

Asn Gly Phe Arg Thr Pro Ser Gly Gly Val Phe Phe Glu Gly Ser Val
      65             70             75             80

```

```

Ala Arg Phe His Cys Gln Asp Gly Phe Lys Leu Lys Gly Ala Thr Lys
      85             90             95

```

```

Arg Leu Cys Leu Lys His Phe Asn Gly Thr Leu Gly Trp Ile Pro Ser
     100             105             110

```

```

Asp Asn Ser Ile Cys Val Gln Glu Asp Cys Arg Ile Pro Gln Ile Glu
     115             120             125

```

```

Asp Ala Glu Ile His Asn Lys Thr Tyr Arg His Gly Glu Lys Leu Ile
     130             135             140

```

```

Ile Thr Cys His Glu Gly Phe Lys Ile Arg Tyr Pro Asp Leu His Asn
     145             150             155             160

```

```

Met Val Ser Leu Cys Arg Asp Asp Gly Thr Trp Asn Asn Leu Pro Ile
      165             170             175

```

```

Cys Gln Gly Cys Leu Arg Pro Leu Ala Ser Ser Asn Gly Tyr Val Asn

```

09909320-071301

180							185					190				
Ile	Ser	Glu	Leu	Gln	Thr	Ser	Phe	Pro	Val	Gly	Thr	Val	Ile	Ser	Tyr	
195							200					205				
Arg	Cys	Phe	Pro	Gly	Phe	Lys	Leu	Asp	Gly	Ser	Ala	Tyr	Leu	Glu	Cys	
210							215					220				
Leu	Gln	Asn	Leu	Ile	Trp	Ser	Ser	Ser	Pro	Pro	Arg	Cys	Leu	Ala	Leu	
225							230					235				
Glu	Ala	Gln	Val	Cys	Pro	Leu	Pro	Pro	Met	Val	Ser	His	Gly	Asp	Phe	
245							250					255				
Val	Cys	His	Pro	Arg	Pro	Cys	Glu	Arg	Tyr	Asn	His	Gly	Thr	Val	Val	
260							265					270				
Glu	Phe	Tyr	Cys	Asp	Pro	Gly	Tyr	Ser	Leu	Thr	Ser	Asp	Tyr	Lys	Tyr	
275							280					285				
Ile	Thr	Cys	Gln	Tyr	Gly	Glu	Trp	Phe	Pro	Ser	Tyr	Gln	Val	Tyr	Cys	
290							295					300				
Ile	Lys	Ser	Glu	Gln	Thr	Trp	Pro	Ser	Thr	His	Glu	Thr	Leu	Leu	Thr	
305							310					315				
Thr	Trp	Lys	Ile	Val	Ala	Phe	Thr	Ala	Thr	Ser	Val	Leu	Leu	Val	Leu	
325							330					335				
Leu	Leu	Val	Ile	Leu	Ala	Arg	Met	Phe	Gln	Thr	Lys	Phe	Lys	Ala	His	
340							345					350				
Phe	Pro	Pro	Arg	Gly	Pro	Pro	Arg	Ser	Ser	Ser	Ser	Asp	Pro	Asp	Phe	
355							360					365				
Val	Val	Val	Asp	Gly	Val	Pro	Val	Met	Leu	Pro	Ser	Tyr	Asp	Glu	Ala	
370							375					380				
Val	Ser	Gly	Gly	Leu	Ser	Ala	Leu	Gly	Pro	Gly	Tyr	Met	Ala	Ser	Val	
385							390					395				
Gly	Gln	Gly	Cys	Pro	Leu	Pro	Val	Asp	Asp	Gln	Ser	Pro	Pro	Ala	Tyr	
405							410					415				
Pro	Gly	Ser	Gly	Asp	Thr	Asp	Thr	Gly	Pro	Gly	Glu	Ser	Glu	Thr	Cys	
420							425					430				
Asp	Ser	Val	Ser	Gly	Ser	Ser	Glu	Leu	Leu	Gln	Ser	Leu	Tyr	Ser	Pro	
435							440					445				
Pro	Arg	Cys	Gln	Glu	Ser	Thr	His	Pro	Ala	Ser	Asp	Asn	Pro	Asp	Ile	
450							455					460				

Ile Ala Ser Thr Ala Glu Glu Val Ala Ser Thr Ser Pro Gly Ile His  
465 470 475 480

His Ala His Trp Val Leu Phe Leu Arg Asn  
485 490

<210> 133

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 133

atctcctatc gctgctttcc cgg

23

<210> 134

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 134

agccaggatc gcagtaaaac tcc

23

<210> 135

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 135

atttaaactt gatgggtctg cgtatcttga gtgcttaca aaccttatct

50

<210> 136

<211> 1815

<212> DNA

<213> Homo sapiens

<400> 136

cccacgcgtc cgctccgcgc cctccccccc gcctcccgctg cggcccgctg gtggcctaga 60  
gatgctgctg ccgcgggttg agttgtcgcg cacgcctctg cccgccagcc cgctccaccg 120  
ccgtagcgcc cgagtgtcgg ggggcgcacc cgagtcgggc catgaggccg ggaaccgcgc 180  
tacaggccgt gctgctggcc gtgctgctgg tggggctgcg ggccgcgacg ggtcgctgc 240  
tgagtgcctc ggatttggac ctcagaggag ggcagccagt ctgccgggga gggacacaga 300

0909320-071801

ggcccttggtta taaagtcatt tacttccatg atacttctcg aagactgaac tttgaggaag 360  
 ccaaagaagc ctgcaggagg gatggaggcc agctagtcag catcgagtct gaagatgaac 420  
 agaaactgat agaaaagttc attgaaaacc tcttgccatc tgatgggtgac ttctggattg 480  
 ggctcaggag gcgtgaggag aaacaaagca atagcacagc ctgccaggac ctttatgctt 540  
 ggactgatgg cagcatatca caatttagga actggtatgt ggatgagccg tcctgcggca 600  
 gcgaggtctg cgtggtcatg taccatcagc catcggcacc cgctggcatc ggaggcccct 660  
 acatgttcca gtggaatgat gaccgggtgca acatgaagaa caatttcatt tgcaaatatt 720  
 ctgatgagaa accagcagtt ccttctagag aagctgaagg tgaggaaaca gagctgacaa 780  
 cacctgtact tccagaagaa acacaggaag aagatgccaa aaaaacattt aaagaaagta 840  
 gagaagctgc cttgaatctg gcctacatcc taatccccag cattccccctt ctccctctcc 900  
 ttgtgggtcac cacagttgta tgttgggttt ggatctgtag aaaaagaaaa cgggagcagc 960  
 cagaccctag cacaagaag caacacacca tctggccctc tcctcaccag ggaaacagcc 1020  
 cggacctaga ggtctacaat gtcataagaa aacaaagcga agctgactta gctgagaccc 1080  
 ggccagacct gaagaatatt tcattccgag tgtgttcggg agaagccact cccgatgaca 1140  
 tgtcttgtga ctatgacaac atggctgtga acccatcaga aagtgggttt gtgactctgg 1200  
 tgagcgtgga gagtggattt gtgaccaatg acatttatga gttctcccca gaccaaatgg 1260  
 ggaggagtaa ggagtctgga tgggtggaaa atgaaatata tggttattag gacatataaa 1320  
 aaactgaaac tgacaacaat ggaaaagaaa tgataagcaa aatcctctta ttttctataa 1380  
 ggaaaataca cagaagggtct atgaacaagc ttagatcagg tcctgtggat gagcatgtgg 1440  
 tccccacgac ctccctgttg accccacagt tttggctgta tcctttatcc cagccagtca 1500  
 tccagctcga ccttatgaga aggtaccttg cccaggtctg gcacatagta gagtctcaat 1560  
 aaatgtcact tggttggttg tatctaactt ttaagggaca gagctttacc tggcagtgat 1620  
 aaagatgggc tgtggagctt ggaaaaccac ctctgttttc cttgctctat acagcagcac 1680  
 atattatcat acagacagaa aatccagaat cttttcaaag cccacatatg gtagcacagg 1740  
 ttggcctgtg catcggcaat tctcatatct gtttttttca aagaataaaa tcaaataaag 1800  
 agcaggaaaa aaaaa 1815

<210> 137

<211> 382

<212> PRT

<213> Homo sapiens

<400> 137

Met Arg Pro Gly Thr Ala Leu Gln Ala Val Leu Leu Ala Val Leu Leu  
 1 5 10 15

Val Gly Leu Arg Ala Ala Thr Gly Arg Leu Leu Ser Ala Ser Asp Leu  
 20 25 30

Asp Leu Arg Gly Gly Gln Pro Val Cys Arg Gly Gly Thr Gln Arg Pro  
 35 40 45

Cys Tyr Lys Val Ile Tyr Phe His Asp Thr Ser Arg Arg Leu Asn Phe  
 50 55 60

Glu Glu Ala Lys Glu Ala Cys Arg Arg Asp Gly Gly Gln Leu Val Ser  
 65 70 75 80

Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile Glu Lys Phe Ile Glu Asn  
 85 90 95

Leu Leu Pro Ser Asp Gly Asp Phe Trp Ile Gly Leu Arg Arg Arg Glu  
 100 105 110



<210> 138

<211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 138  
 gttcattgaa aacctcttgc catctgatgg tgacttctgg attgggctca 50

<210> 139  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 139  
 aagccaaaga agcctgcagg aggg 24

<210> 140  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 140  
 cagtccaagc ataaagggtcc tggc 24

<210> 141  
 <211> 1514  
 <212> DNA  
 <213> Homo sapiens

<400> 141  
 ggggtctccc tcagggccgg gaggcacagc ggtccctgct tgctgaaggg ctggatgtac 60  
 gcatccgcag gttcccgcgg acttgggggc gcccgctgag ccccggcgcc cgcagaagac 120  
 ttgtgtttgc ctctgcagc ctcaacccgg agggcagcga gggcctacca ccatgatcac 180  
 tgggtgtgttc agcatgcgct tgtggacccc agtgggcgctc ctgacctcgc tggcgactctg 240  
 cctgcaccag cggcgggtgg ccctggccga gctgcaggag gccgatggcc agtgtccggt 300  
 cgaccgcagc ctgctgaagt tgaaaatggt gcaggtcgtg tttcgacacg gggctcggag 360  
 tcctctcaag ccgctcccgc tggaggagca ggtagagtgg aacccccagc tattagaggt 420  
 cccaccccaa actcagtttg attacacagt caccaatcta gctggtggtc cgaaaccata 480  
 ttctccttac gactctcaat accatgagac caccctgaag gggggcatgt ttgctgggca 540  
 gctgaccaag gtgggcatgc agcaaatggt tgccttggga gagagactga ggaagaacta 600  
 tgtggaagac attccctttc tttcaccaac cttcaaccca caggaggtct ttattcgttc 660  
 cactaacatt tttcgggaatc tggagtccac ccgttggttg ctggctgggc tttccagtg 720

```

tcagaaagaa ggacccatca tcatccacac tgatgaagca gattcagaag tcttgatatcc 780
caactaccaa agctgctgga gcctgaggca gagaaccaga ggccggaggc agactgcctc 840
tttacagcca ggaatctcag aggatttgaa aaagggtgaag gacaggatgg gcattgacag 900
tagtgataaa gtggacttct tcatcctcct ggacaacgtg gctgccgagc aggcacacaa 960
cctcccaagc tgcccatgc tgaagagatt tgcacggatg atcgaacaga gagctgtgga 1020
cacatccttg tacatactgc ccaaggaaga cagggaagt cttcagatgg cagtaggccc 1080
attcctccac atcctagaga gcaacctgct gaaagccatg gactctgcca ctgccccga 1140
caagatcaga aagctgtatc tctatgcggc tcatgatgtg accttcatac cgctcttaat 1200
gacctgggg atttttgacc acaaattggc accgtttgct gttgacctga ccatggaact 1260
ttaccagcac ctggaatcta aggagtgggt tgtgcagctc tattaccacg ggaaggagca 1320
ggtgccgaga gggtgccctg atgggctctg cccgctggac atgttcttga atgccatgtc 1380
agtttatacc ttaagccag aaaaatacca tgcactctgc tctcaaactc aggtgatgga 1440
agttggaaat gaagagtaac tgatttataa aagcaggatg tgttgatttt aaaataaagt 1500
gcctttatac aatg 1514

```

<210> 142

<211> 428

<212> PRT

<213> Homo sapiens

<400> 142

```

Met Ile Thr Gly Val Phe Ser Met Arg Leu Trp Thr Pro Val Gly Val
  1              5              10              15

Leu Thr Ser Leu Ala Tyr Cys Leu His Gln Arg Arg Val Ala Leu Ala
      20              25              30

Glu Leu Gln Glu Ala Asp Gly Gln Cys Pro Val Asp Arg Ser Leu Leu
      35              40              45

Lys Leu Lys Met Val Gln Val Val Phe Arg His Gly Ala Arg Ser Pro
      50              55              60

Leu Lys Pro Leu Pro Leu Glu Glu Gln Val Glu Trp Asn Pro Gln Leu
      65              70              75              80

Leu Glu Val Pro Pro Gln Thr Gln Phe Asp Tyr Thr Val Thr Asn Leu
      85              90              95

Ala Gly Gly Pro Lys Pro Tyr Ser Pro Tyr Asp Ser Gln Tyr His Glu
      100              105              110

Thr Thr Leu Lys Gly Gly Met Phe Ala Gly Gln Leu Thr Lys Val Gly
      115              120              125

Met Gln Gln Met Phe Ala Leu Gly Glu Arg Leu Arg Lys Asn Tyr Val
      130              135              140

Glu Asp Ile Pro Phe Leu Ser Pro Thr Phe Asn Pro Gln Glu Val Phe
      145              150              155              160

Ile Arg Ser Thr Asn Ile Phe Arg Asn Leu Glu Ser Thr Arg Cys Leu
      165              170              175

```

Leu Ala Gly Leu Phe Gln Cys Gln Lys Glu Gly Pro Ile Ile Ile His  
 180 185 190  
 Thr Asp Glu Ala Asp Ser Glu Val Leu Tyr Pro Asn Tyr Gln Ser Cys  
 195 200 205  
 Trp Ser Leu Arg Gln Arg Thr Arg Gly Arg Arg Gln Thr Ala Ser Leu  
 210 215 220  
 Gln Pro Gly Ile Ser Glu Asp Leu Lys Lys Val Lys Asp Arg Met Gly  
 225 230 235 240  
 Ile Asp Ser Ser Asp Lys Val Asp Phe Phe Ile Leu Leu Asp Asn Val  
 245 250 255  
 Ala Ala Glu Gln Ala His Asn Leu Pro Ser Cys Pro Met Leu Lys Arg  
 260 265 270  
 Phe Ala Arg Met Ile Glu Gln Arg Ala Val Asp Thr Ser Leu Tyr Ile  
 275 280 285  
 Leu Pro Lys Glu Asp Arg Glu Ser Leu Gln Met Ala Val Gly Pro Phe  
 290 295 300  
 Leu His Ile Leu Glu Ser Asn Leu Leu Lys Ala Met Asp Ser Ala Thr  
 305 310 315 320  
 Ala Pro Asp Lys Ile Arg Lys Leu Tyr Leu Tyr Ala Ala His Asp Val  
 325 330 335  
 Thr Phe Ile Pro Leu Leu Met Thr Leu Gly Ile Phe Asp His Lys Trp  
 340 345 350  
 Pro Pro Phe Ala Val Asp Leu Thr Met Glu Leu Tyr Gln His Leu Glu  
 355 360 365  
 Ser Lys Glu Trp Phe Val Gln Leu Tyr Tyr His Gly Lys Glu Gln Val  
 370 375 380  
 Pro Arg Gly Cys Pro Asp Gly Leu Cys Pro Leu Asp Met Phe Leu Asn  
 385 390 395 400  
 Ala Met Ser Val Tyr Thr Leu Ser Pro Glu Lys Tyr His Ala Leu Cys  
 405 410 415  
 Ser Gln Thr Gln Val Met Glu Val Gly Asn Glu Glu  
 420 425

&lt;210&gt; 143

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

F08720"02E660

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 143

ccaactacca aagctgctgg agcc

24

<210> 144

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 144

gcagctctat taccacggga agga

24

<210> 145

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 145

tccttcccgt ggtaatagag ctgc

24

<210> 146

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 146

ggcagagaac cagaggccgg aggagactgc ctctttacag ccagg

45

<210> 147

<211> 1686

<212> DNA

<213> Homo sapiens

<400> 147

ctcctcttaa catacttgca gctaaaacta aatattgctg cttggggacc tccttctagc 60  
cttaaatttc agtcatcac cttcacctgc cttgggtcatg gctctgctat tctccttgat 120  
ccttgccatt tgcaccagac ctggattcct agcgtctcca tctggagtgc ggctggtggg 180

0909330.071801

```

<210> 148
<211> 347
<212> PRT
<213> Homo sapiens

<400> 148
Met Ala Leu Leu Phe Ser Leu Ile Leu Ala Ile Cys Thr Arg Pro Gly
  1                               10                      15
Phe Leu Ala Ser Pro Ser Gly Val Arg Leu Val Gly Gly Leu His Arg
  20                          25                      30
Cys Glu Gly Arg Val Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val
  35                          40                      45
Cys Asp Asp Gly Trp Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu
  50                          55                      60
Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu
  65                          70                      75                      80
Pro Pro Ala Glu Lys Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys
  85                          90                      95
Thr Gly Thr Glu Asp Thr Leu Ala Gln Cys Glu Gln Glu Glu Val Tyr
  100                        105                      110

```

Asp Cys Ser His Asp Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu  
 115 120 125  
 Ser Ser Phe Ser Pro Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro  
 130 135 140  
 Gly His Cys Lys Gly Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr  
 145 150 155 160  
 Thr Val Cys Gln Thr Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys  
 165 170 175  
 Arg Gln Leu Gly Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn  
 180 185 190  
 Lys His Ala Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys  
 195 200 205  
 Ser Gly Arg Glu Ala Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly  
 210 215 220  
 Lys Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp  
 225 230 235 240  
 Pro Phe Asp Leu Arg Leu Val Gly Gly Asp Asn Leu Cys Ser Gly Arg  
 245 250 255  
 Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn  
 260 265 270  
 Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly  
 275 280 285  
 Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly  
 290 295 300  
 Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln  
 305 310 315 320  
 Ser Leu Glu Gln Cys Gln His Arg Phe Trp Gly Phe His Asp Cys Thr  
 325 330 335  
 His Gln Glu Asp Val Ala Val Ile Cys Ser Val  
 340 345

<210> 149

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

09909330-071601

## oligonucleotide probe

<400> 149  
 ttcagctcat caccttcacc tgcc 24

<210> 150  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 150  
 ggctcataca aaataccact aggg 24

<210> 151  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 151  
 gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt 50

<210> 152  
 <211> 1427  
 <212> DNA  
 <213> Homo sapiens

<400> 152  
 actgcactcg gttctatcga ttgaattccc cggggatcct ctagagatcc ctcgacctcg 60  
 acccacgcgt ccgcggacgc gtgggcggac gcgtgggccg gctaccagga agagtctgcc 120  
 gaaggtgaag gccatggact tcatcacctc cacagccatc ctgcccctgc tggtcggctg 180  
 cctgggcgtc ttccggcctct tccggctgct gcagtgggtg cgcgggaagg cctacctgcg 240  
 gaatgctgtg gtggtgatca caggcgccac ctccaggctg ggcaaaagaat gtgcaaaagt 300  
 cttctatgct gcgggtgcta aactgggtgct ctgtggcccg aatgggtggg ccctagaaga 360  
 gctcatcaga gaacttaccg cttctcatgc caccaagggtg cagacacaca agccttactt 420  
 ggtgaccttc gacctcacag actctggggc catagtgtgca gcagcagctg agatcctgca 480  
 gtgctttggc tatgtcgaca tacttgtcaa caatgctggg atcagctacc gtggtaccat 540  
 catggacacc acagtggatg tggacaagag ggtcatggag acaaactact ttggcccagt 600  
 tgctctaacg aaagcactcc tgccctccat gatcaagagg aggcaaggcc acattgtcgc 660  
 catcagcagc atccagggca agatgagcat tccttttcga tcagcatatg cagcctccaa 720  
 gcacgcgaacc caggctttct ttgactgtct gcgtgccgag atggaacagt atgaaattga 780  
 ggtgaccgtc atcagccccg gctacatcca caccaacctc tctgtaaagt ccatcaccgc 840  
 ggatggatct aggtatggag ttatggacac caccacagcc cagggccgaa gccctgtgga 900  
 ggtggcccag gatgttcttg ctgctgtggg gaagaagaag aaagatgtga tcctggctga 960  
 cttactgcct tccttggtctg tttatcttcg aactctggct cctgggctct tcttcagcct 1020  
 catggcctcc agggccagaa aagagcggaa atccaagaac tcctagtact ctgaccagcc 1080



```
<210> 153
<211> 310
<212> PRT
<213> Homo sapiens
```

Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys  
1 5 10 15

Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly  
35 40 45

Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu  
65 70 75 80

Val Thr Phe Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala Ala  
100 105 110

Gly Ile Ser Tyr Arg Gly Thr Ile Met Asp Thr Thr Val Asp Val Asp  
130 135 140

Ala Leu Leu Pro Ser Met Ile Lys Arg Arg Gln Gly His Ile Val Ala  
165 170 175

Ala Ala Ser Lys His Ala Thr Gln Ala Phe Phe Asp Cys Leu Arg Ala  
195 200 205

Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr

20

<400> 156  
tcatactggt ccatctcggc acgc 24

<210> 157  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 157  
aatggtgggg ccctagaaga gctcatcaga gaactcaccg cttctcatgc 50

<210> 158  
<211> 1771  
<212> DNA  
<213> Homo sapiens

<400> 158  
cccacgcgtc cgctggtggt agatcgagca accctctaaa agcagtttag agtggttaaaa 60  
aaaaaaaaaa acacaccaa cgctcgagc caaaaagg atgaaatttc ttctggacat 120  
cctcctgctt ctcccggttac tgatcgcttg ctccctagag tccttcgtga agctttttat 180  
tcctaagagg agaaaatcag tcaccggcga aatcggtgctg attacaggag ctgggcatgg 240  
aattgggaga ctgactgcct atgaatttgc taaacttaaa agcaagctgg ttctctggga 300  
tataaataag catggactgg aggaaacagc tgccaaatgc aagggactgg gtgccaagg 360  
tcataccttt gtggtagact gcagcaaccg agaagatatt tacagctctg caaagaagg 420  
gaaggcagaa attggagatg ttagtatttt agtaaataat gctggtgtag tctatacatc 480  
agatttggtt gctacacaag atcctcagat tgaaaagact tttgaagtta atgtacttgc 540  
acatttctgg actacaaagg catttcttcc tgcaatgacg aagaataacc atggccatat 600  
tgtcactgtg gcttcggcag ctggacatgt ctcggtcccc ttcttactgg cttactgttc 660  
aagcaagttt gctgctgttg gatttcataa aactttgaca gatgaactgg ctgccttaca 720  
aataactgga gtcaaaacaa catgtctgtg tcctaatttc gtaaacactg gcttcatcaa 780  
aatccaagt acaagtttgg gaccactctt ggaacctgag gaagtggtaa acaggctgat 840  
gcatgggatt ctgactgagc agaagatgat ttttattcca tcttctatag cttttttaac 900  
aacattggaa aggatccttc ctgagcgttt cctggcagtt ttaaaacgaa aaatcagtgt 960  
taagtttgat gcagttattg gatataaaat gaaagcgcaa taagcaccta gttttctgaa 1020  
aactgattta ccaggttttag gttgatgtca tctaatagtg ccagaatttt aatgtttgaa 1080  
cttctgtttt ttctaattat cccattttct tcaatatcat ttttgaggct ttggcagtct 1140  
tcatttacta ccacttggtt tttagccaaa agctgattac atatgatata aacagagaaa 1200  
tacctttaga ggtgacttta aggaaaatga agaaaaagaa ccaaaatgac tttattaaaa 1260  
taatttccaa gattatttgg ggctcacctg aaggctttgc aaaatttcta ccataaccgt 1320  
ttatttaaca tatattttta tttttgattg cacttaaatt ttgtataatt tgtgtttctt 1380  
tttctgttct acataaaatc agaaacttca agctctctaa ataaaaatgaa ggactatatc 1440  
tagtgggtatt tcacaatgaa tatcatgaac tctcaatggg taggtttcat cctaccatt 1500  
gccactctgt ttcttgagag atacctcaca ttccaatgcc aaacatttct gcacagggaa 1560  
gctagagggtg gatacacgtg ttgcaagtat aaaagcatca ctgggattta aggagaattg 1620  
agagaatgta ccacacaaatg gcagcaataa taaatggatc aactttaaaa aaaaaaaaaa 1680  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1740  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a a 1771

<210> 159

<211> 300  
 <212> PRT  
 <213> Homo sapiens

<400> 159

Met	Lys	Phe	Leu	Leu	Asp	Ile	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Ile	Val
1				5					10					15	
Cys	Ser	Leu	Glu	Ser	Phe	Val	Lys	Leu	Phe	Ile	Pro	Lys	Arg	Arg	Lys
			20					25					30		
Ser	Val	Thr	Gly	Glu	Ile	Val	Leu	Ile	Thr	Gly	Ala	Gly	His	Gly	Ile
		35					40					45			
Gly	Arg	Leu	Thr	Ala	Tyr	Glu	Phe	Ala	Lys	Leu	Lys	Ser	Lys	Leu	Val
	50					55					60				
Leu	Trp	Asp	Ile	Asn	Lys	His	Gly	Leu	Glu	Glu	Thr	Ala	Ala	Lys	Cys
	65				70					75					80
Lys	Gly	Leu	Gly	Ala	Lys	Val	His	Thr	Phe	Val	Val	Asp	Cys	Ser	Asn
				85					90					95	
Arg	Glu	Asp	Ile	Tyr	Ser	Ser	Ala	Lys	Lys	Val	Lys	Ala	Glu	Ile	Gly
			100					105					110		
Asp	Val	Ser	Ile	Leu	Val	Asn	Asn	Ala	Gly	Val	Val	Tyr	Thr	Ser	Asp
		115					120					125			
Leu	Phe	Ala	Thr	Gln	Asp	Pro	Gln	Ile	Glu	Lys	Thr	Phe	Glu	Val	Asn
	130					135					140				
Val	Leu	Ala	His	Phe	Trp	Thr	Thr	Lys	Ala	Phe	Leu	Pro	Ala	Met	Thr
	145				150					155					160
Lys	Asn	Asn	His	Gly	His	Ile	Val	Thr	Val	Ala	Ser	Ala	Ala	Gly	His
			165					170						175	
Val	Ser	Val	Pro	Phe	Leu	Leu	Ala	Tyr	Cys	Ser	Ser	Lys	Phe	Ala	Ala
			180					185					190		
Val	Gly	Phe	His	Lys	Thr	Leu	Thr	Asp	Glu	Leu	Ala	Ala	Leu	Gln	Ile
		195					200					205			
Thr	Gly	Val	Lys	Thr	Thr	Cys	Leu	Cys	Pro	Asn	Phe	Val	Asn	Thr	Gly
	210					215					220				
Phe	Ile	Lys	Asn	Pro	Ser	Thr	Ser	Leu	Gly	Pro	Thr	Leu	Glu	Pro	Glu
	225				230					235					240
Glu	Val	Val	Asn	Arg	Leu	Met	His	Gly	Ile	Leu	Thr	Glu	Gln	Lys	Met
				245					250					255	

05909320-071301

Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu Arg Ile  
 260 265 270

Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile Ser Val Lys  
 275 280 285

Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln  
 290 295 300

<210> 160

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 160

ggtgaaggca gaaattggag atg

23

<210> 161

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 161

atcccatgca tcagcctggt tacc

24

<210> 162

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 162

gctggtgtag tctatacatc agatttggtt gctacacaag atcctcag

48

<210> 163

<211> 2076

<212> DNA

<213> Homo sapiens

<400> 163

cccacgcgtc cgcggacgcg tgggtcgact agttctagat cgcgagcggc cgcccgcggc 60  
 tcagggagga gcaccgactg cgccgcaccc tgagagatgg ttggtgccat gtggaagggtg 120

1.03E20.02E0560

attgttttcgc tggctcctggt gatgcctggc cctgtgatg ggctgttttcg ctccctatac 180  
 agaagtgttt ccatgccacc taagggagac tcaggacagc cattatttct caccctttac 240  
 attgaagctg ggaagatcca aaaaggaaga gaattgagtt tggctcggccc tttcccagga 300  
 ctgaacatga agagtattgc cggcttcctc accgtgaata agacttaca cagcaacctc 360  
 ttcttctggt tcttcccagc tcagatacag ccagaagatg cccagtagt tctctggcta 420  
 caggggtgggc cgggaggttc atccatgttt ggactccttg tggaacatgg gccttatggt 480  
 gtcacaagta acatgacctt gcgtgacaga gacttcccct ggaccacaac gctctccatg 540  
 ctttacattg acaatccagt gggcacaggc ttcagtttta ctgatgatac ccacggatat 600  
 gcagtcaatg aggacgatgt agcacgggat ttatacagt cactaattca gtttttccag 660  
 atatttctctg aatataaaaa taatgacttt tatgtcactg gggagtctta tgcagggaaa 720  
 tatgtgccag ccattgcaca cctcatccat tccctcaacc ctgtgagaga ggtgaagatc 780  
 aacctgaacg gaattgctat tggagatgga tattctgatc ccgaatcaat tatagggggc 840  
 tatgcagaat tcctgtacca aattggcttg ttggatgaga agcaaaaaaa gtacttccag 900  
 aagcagtgcc atgaatgcat agaacacatc aggaagcaga actgggttga ggcctttgaa 960  
 atactggata aactactaga tggcgactta acaagtgatc cttcttactt ccagaatggt 1020  
 acaggatgta gtaattacta taactttttg cgggtgcacgg aacctgagga tcagctttac 1080  
 tatgtgaaat ttttgtcact ccagaggtg agacaagcca tccacgtggg gaatcagact 1140  
 tttaatgatg gaactatagt tgaaaagtac ttgcgagaag atacagtaca gtcagttaag 1200  
 ccatggttaa ctgaaatcat gaataattat aagggttctga tctacaatgg ccaactggac 1260  
 atcatcgtgg agactgcctt gacagagcgc tccttgatgg gcatggactg gaaaggatcc 1320  
 caggaataca agaaggcaga aaaaaaagtt tggaagatct taaatctga cagtgaagtg 1380  
 gctgggttaca tccggcaagc ggggtgacttc catcaggtaa ttattcgagg tggaggacat 1440  
 attttacctt atgaccagcc tctgagagct tttgacatga ttaatcgatt catttatgga 1500  
 aaaggatggg atccttatgt tggataaact accttcccaa aagagaacat cagaggtttt 1560  
 cattgttgaa aagaaaatcg taaaaacaga aaatgtcata ggaataaaaa aattatcttt 1620  
 tcatatctgc aagatttttt tcatcaataa aaattatcct tgaaacaagt gagcttttgt 1680  
 ttttgggggg agatgtttac tacaaaatta acatgagtac atgagtaaga attacattat 1740  
 ttaacttaaa ggatgaaagg tatggatgat gtgacactga gacaagatgt ataaatgaaa 1800  
 ttttaggggtc ttgaatagga agttttaatt tcttctaaga gtaagtgaaa agtgcagttg 1860  
 taacaaacaa agctgtaaca tctttttctg ccaataacag aagtttggca tgccgtgaag 1920  
 gtgttttgaa atattattgg ataagaatag ctcaattatc ccaataaaat ggatgaagct 1980  
 ataatagttt tggggaaaaag attctcaaat gtataaagtc ttagaacaaa agaattcttt 2040  
 gaaataaaaa tattatatat aaaagtaaaa aaaaaa 2076

<210> 164

<211> 476

<212> PRT

<213> Homo sapiens

<400> 164

Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu Met  
 1 5 10 15

Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser Val Ser  
 20 25 30

Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr  
 35 40 45

Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly  
 50 55 60

Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val

65					70					75				80	
Asn	Lys	Thr	Tyr	Asn	Ser	Asn	Leu	Phe	Phe	Trp	Phe	Phe	Pro	Ala	Gln
				85					90					95	
Ile	Gln	Pro	Glu	Asp	Ala	Pro	Val	Val	Leu	Trp	Leu	Gln	Gly	Gly	Pro
			100					105					110		
Gly	Gly	Ser	Ser	Met	Phe	Gly	Leu	Phe	Val	Glu	His	Gly	Pro	Tyr	Val
		115					120					125			
Val	Thr	Ser	Asn	Met	Thr	Leu	Arg	Asp	Arg	Asp	Phe	Pro	Trp	Thr	Thr
	130					135					140				
Thr	Leu	Ser	Met	Leu	Tyr	Ile	Asp	Asn	Pro	Val	Gly	Thr	Gly	Phe	Ser
145					150				155						160
Phe	Thr	Asp	Asp	Thr	His	Gly	Tyr	Ala	Val	Asn	Glu	Asp	Asp	Val	Ala
				165				170						175	
Arg	Asp	Leu	Tyr	Ser	Ala	Leu	Ile	Gln	Phe	Phe	Gln	Ile	Phe	Pro	Glu
		180					185						190		
Tyr	Lys	Asn	Asn	Asp	Phe	Tyr	Val	Thr	Gly	Glu	Ser	Tyr	Ala	Gly	Lys
	195						200					205			
Tyr	Val	Pro	Ala	Ile	Ala	His	Leu	Ile	His	Ser	Leu	Asn	Pro	Val	Arg
	210					215					220				
Glu	Val	Lys	Ile	Asn	Leu	Asn	Gly	Ile	Ala	Ile	Gly	Asp	Gly	Tyr	Ser
225				230				235						240	
Asp	Pro	Glu	Ser	Ile	Ile	Gly	Gly	Tyr	Ala	Glu	Phe	Leu	Tyr	Gln	Ile
				245				250						255	
Gly	Leu	Leu	Asp	Glu	Lys	Gln	Lys	Lys	Tyr	Phe	Gln	Lys	Gln	Cys	His
		260					265					270			
Glu	Cys	Ile	Glu	His	Ile	Arg	Lys	Gln	Asn	Trp	Phe	Glu	Ala	Phe	Glu
	275						280					285			
Ile	Leu	Asp	Lys	Leu	Leu	Asp	Gly	Asp	Leu	Thr	Ser	Asp	Pro	Ser	Tyr
	290					295					300				
Phe	Gln	Asn	Val	Thr	Gly	Cys	Ser	Asn	Tyr	Tyr	Asn	Phe	Leu	Arg	Cys
305					310				315					320	
Thr	Glu	Pro	Glu	Asp	Gln	Leu	Tyr	Tyr	Val	Lys	Phe	Leu	Ser	Leu	Pro
				325				330					335		
Glu	Val	Arg	Gln	Ala	Ile	His	Val	Gly	Asn	Gln	Thr	Phe	Asn	Asp	Gly
		340					345						350		

T03T20"02E60650

Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys  
355 360 365

Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn  
370 375 380

Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu Arg Ser Leu  
385 390 395 400

Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys  
405 410 415

Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile  
420 425 430

Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly Gly His  
435 440 445

Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn Arg  
450 455 460

Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly  
465 470 475

<210> 165

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 165

ttccatgcca cctaaggag actc

24

<210> 166

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 166

tgcatgaggt gtgcaatggc tggc

24

<210> 167

<211> 24

<212> DNA

<213> Artificial Sequence

09909320-071801



&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 167

agctctcaga ggctgggtcat aggg

24

&lt;210&gt; 168

&lt;211&gt; 50

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 168

gtcggccctt tcccaggact gaacatgaag agttatgccg gcttccctcac

50

&lt;210&gt; 169

&lt;211&gt; 2477

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 169

cgagggtctt tccgggtccg gaatggcaca tgtgggaatc ccagtcttgt tggctacaac 60  
 atttttccct ttctaacaa gttctaacag ctgttctaac agctagtgat caggggttct 120  
 tcttgctgga gaagaaaggg ctgagggcag agcagggcac tctcactcag ggtgaccagc 180  
 tccttgccctc tctgtggata acagagcatg agaaagtga gagatgcagc ggagtgaggt 240  
 gatggaagtc taaaatagga aggaattttg tgtgcaatat cagactctgg gagcagttga 300  
 cctggagagc ctggggggagg gcctgcctaa caagctttca aaaaacagga ggcacttcca 360  
 ctgggctggg ataagacgtg ccggtaggat agggaagact ggggtttagt ctaatatcaa 420  
 attgactggc tgggtgaact tcaacagcct tttaacctct ctgggagatg aaaacgatgg 480  
 cttaaggggc cagaaataga gatgctttgt aaaataaaat tttaaaaaaa gcaagtattt 540  
 tatagcataa aggctagaga ccaaaataga taacaggatt ccctgaacat tcctaagagg 600  
 gagaaagtat gttaaaaata gaaaaaccaa aatgcagaag gaggagactc acagagctaa 660  
 accaggatgg ggaccctggg tcaggccagc ctctttgctc ctcccggaaa ttatttttgg 720  
 tctgaccact ctgccttgtg ttttgagaa tcatgtgagg gccaacggg gaaggtggag 780  
 cagatgagca cacacaggag ccgtctcctc accgcgcgcc ctctcagcat ggaacagagg 840  
 cagccctggc cccgggccct ggaggtggac agcgcctctg tggctctgct ctcagtggtc 900  
 tgggtgctgc tggccccccc agcagccggc atgcctcagt tcagcacctt ccactctgag 960  
 aatcgtgact ggaccttcaa ccacttgacc gtccaccaag ggacgggggc cgtctatgtg 1020  
 ggggccatca accgggtcta taagctgaca ggcaacctga ccatccaggt ggctcataag 1080  
 acagggccag aagaggacaa caagtctcgt taccgcgcc tcactcgtgca gccctgcagc 1140  
 gaagtgtca ccctaccaaa caatgtcaac aagctgctca tcattgacta ctctgagaac 1200  
 cgcctgctgg cctgtgggag cctctaccag ggggtctgca agctgctgcg gctggatgac 1260  
 ctcttcatcc tgggtggagcc atcccacaag aaggagcact acctgtccag tgtcaacaag 1320  
 acgggcacca tgtacggggt gattgtgcgc tctgaggggt aggatggcaa gctcttcatc 1380  
 ggcacggctg tggatgggaa gcaggattac ttcccagccc tgtccagccg gaagctgccc 1440  
 cgagaccctg agtcctcagc catgctcgac tatgagctac acagcgattt tgtctcctct 1500  
 ctcatcaaga tccttccaga caccctggcc ctggtctccc actttgacat cttctacatc 1560  
 tacggctttg ctagtggggg ctttgtctac tttctcactg tccagcccga gaccctgag 1620  
 ggtgtggcca tcaactccgc tggagacctc ttctacacct cagcatcgt gcggctctgc 1680

aaggatgacc ccaagttcca ctcatagctg tccctgccct tcggtgcac ccggggccggg 1740  
gtggaataacc gcctcctgca ggctgcttac ctggccaagc ctggggactc actggcccag 1800  
gccttcaata tcaccagcca ggacgatgta ctctttgcca tcttctccaa agggcagaag 1860  
cagtatcacc acccgcccga tgactctgcc ctgtgtgcct tccctatccg ggccatcaac 1920  
ttgcagatca aggagcgct gcagtcctgc taccagggcg agggcaacct ggagctcaac 1980  
tggctgctgg ggaaggacgt ccagtgcacg aaggcgctg tccccatcga tgataacttc 2040  
tgtggactgg acatcaacca gccctggga ggctcaactc cagtggaggg cctgacctg 2100  
tacaccacca gcagggaccg catgacctct gtggcctcct acgtttacaa cggctacagc 2160  
gtgggtttttg tggggactaa gagtggcaag ctgaaaaagg taagagtcta tgagttcaga 2220  
tgctccaatg ccattcacct cctcagcaaa gagtccctct tgggaaggtag ctattggtgg 2280  
agatttaact ataggcaact ttattttctt ggggaacaaa ggtgaaatgg ggaggtaga 2340  
aggggttaat tttgtgactt agcttctagc tacttcctcc agccatcagt cattgggtat 2400  
gtaaggaatg caagcgattt tcaatatttc ccaaacttta agaaaaaact ttaagaaggt 2460  
acatctgcaa aagcaaa 2477

<210> 170

<211> 552

<212> PRT

<213> Homo sapiens

<400> 170

Met Gly Thr Leu Gly Gln Ala Ser Leu Phe Ala Pro Pro Gly Asn Tyr  
1 5 10 15

Phe Trp Ser Asp His Ser Ala Leu Cys Phe Ala Glu Ser Cys Glu Gly  
20 25 30

Gln Pro Gly Lys Val Glu Gln Met Ser Thr His Arg Ser Arg Leu Leu  
35 40 45

Thr Ala Ala Pro Leu Ser Met Glu Gln Arg Gln Pro Trp Pro Arg Ala  
50 55 60

Leu Glu Val Asp Ser Arg Ser Val Val Leu Leu Ser Val Val Trp Val  
65 70 75 80

Leu Leu Ala Pro Pro Ala Ala Gly Met Pro Gln Phe Ser Thr Phe His  
85 90 95

Ser Glu Asn Arg Asp Trp Thr Phe Asn His Leu Thr Val His Gln Gly  
100 105 110

Thr Gly Ala Val Tyr Val Gly Ala Ile Asn Arg Val Tyr Lys Leu Thr  
115 120 125

Gly Asn Leu Thr Ile Gln Val Ala His Lys Thr Gly Pro Glu Glu Asp  
130 135 140

Asn Lys Ser Arg Tyr Pro Pro Leu Ile Val Gln Pro Cys Ser Glu Val  
145 150 155 160

Leu Thr Leu Thr Asn Asn Val Asn Lys Leu Leu Ile Ile Asp Tyr Ser  
165 170 175

09909320-071801

Glu Asn Arg Leu Leu Ala Cys Gly Ser Leu Tyr Gln Gly Val Cys Lys  
 180 185 190  
 Leu Leu Arg Leu Asp Asp Leu Phe Ile Leu Val Glu Pro Ser His Lys  
 195 200 205  
 Lys Glu His Tyr Leu Ser Ser Val Asn Lys Thr Gly Thr Met Tyr Gly  
 210 215 220  
 Val Ile Val Arg Ser Glu Gly Glu Asp Gly Lys Leu Phe Ile Gly Thr  
 225 230 235 240  
 Ala Val Asp Gly Lys Gln Asp Tyr Phe Pro Thr Leu Ser Ser Arg Lys  
 245 250 255  
 Leu Pro Arg Asp Pro Glu Ser Ser Ala Met Leu Asp Tyr Glu Leu His  
 260 265 270  
 Ser Asp Phe Val Ser Ser Leu Ile Lys Ile Pro Ser Asp Thr Leu Ala  
 275 280 285  
 Leu Val Ser His Phe Asp Ile Phe Tyr Ile Tyr Gly Phe Ala Ser Gly  
 290 295 300  
 Gly Phe Val Tyr Phe Leu Thr Val Gln Pro Glu Thr Pro Glu Gly Val  
 305 310 315 320  
 Ala Ile Asn Ser Ala Gly Asp Leu Phe Tyr Thr Ser Arg Ile Val Arg  
 325 330 335  
 Leu Cys Lys Asp Asp Pro Lys Phe His Ser Tyr Val Ser Leu Pro Phe  
 340 345 350  
 Gly Cys Thr Arg Ala Gly Val Glu Tyr Arg Leu Leu Gln Ala Ala Tyr  
 355 360 365  
 Leu Ala Lys Pro Gly Asp Ser Leu Ala Gln Ala Phe Asn Ile Thr Ser  
 370 375 380  
 Gln Asp Asp Val Leu Phe Ala Ile Phe Ser Lys Gly Gln Lys Gln Tyr  
 385 390 395 400  
 His His Pro Pro Asp Asp Ser Ala Leu Cys Ala Phe Pro Ile Arg Ala  
 405 410 415  
 Ile Asn Leu Gln Ile Lys Glu Arg Leu Gln Ser Cys Tyr Gln Gly Glu  
 420 425 430  
 Gly Asn Leu Glu Leu Asn Trp Leu Leu Gly Lys Asp Val Gln Cys Thr  
 435 440 445  
 Lys Ala Pro Val Pro Ile Asp Asp Asn Phe Cys Gly Leu Asp Ile Asn

09009320-071801  
 100720-02E00660

450                      455                      460  
 Gln Pro Leu Gly Gly Ser Thr Pro Val Glu Gly Leu Thr Leu Tyr Thr  
 465                      470                      475                      480  
 Thr Ser Arg Asp Arg Met Thr Ser Val Ala Ser Tyr Val Tyr Asn Gly  
                     485                      490                      495  
 Tyr Ser Val Val Phe Val Gly Thr Lys Ser Gly Lys Leu Lys Lys Val  
                     500                      505                      510  
 Arg Val Tyr Glu Phe Arg Cys Ser Asn Ala Ile His Leu Leu Ser Lys  
                     515                      520                      525  
 Glu Ser Leu Leu Glu Gly Ser Tyr Trp Trp Arg Phe Asn Tyr Arg Gln  
                     530                      535                      540  
 Leu Tyr Phe Leu Gly Glu Gln Arg  
 545                      550

<210> 171

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 171

tggaataaccg cctcctgcag

20

<210> 172

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 172

cttctgccct ttggagaaga tggc

24

<210> 173

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

108720-02E60660

<400> 173  
ggactcactg gccaggcct tcaatatcac cagccaggac gat 42

<210> 174  
<211> 3106  
<212> DNA  
<213> Homo sapiens

<220>  
<221> modified\_base  
<222> (1683)  
<223> a, t, c or g

<400> 174  
aggctccccg gcgcggctga gtgcggactg gagtgggaac ccgggtcccc gcgcttagag 60  
aacacgcgat gaccacgtgg agcctccggc ggaggccggc ccgcacgctg ggactcctgc 120  
tgctggctgt cttgggcttc ctgggtctcc gcaggctgga ctggagcacc ctggtccctc 180  
tgcggtcccg ccatcgacag ctggggctgc aggccaaagg ctggaacttc atgctggagg 240  
attccacctt ctggatcttc gggggctcca tccactattt ccgtgtgccc agggagtact 300  
ggagggaccg cctgctgaag atgaaggcct gtggcttgaa caccctcacc acctatgttc 360  
cgtggaacct gcatgagcca gaaagaggca aatttgactt ctctgggaac ctggacctgg 420  
aggccttcgt cctgatggcc gcagagatcg ggctgtgggt gattctgctg ccaggccccct 480  
acatctgcag tgagatggac ctcgggggct tgcccagctg gctactccaa gacctggca 540  
tgaggctgag gacaacttac aagggttca ccgaagcagt ggacctttat tttgaccacc 600  
tgatgtccag ggtggtgcca ctccagtaca agcgtggggg acctatcatt gccgtgcagg 660  
tgagaaatga atatggttcc tataataaag accccgcata catgccctac gtcaagaagg 720  
cactggagga ccgtggcatt gtggaactgc tcctgacttc agacaacaag gatgggctga 780  
gcaaggggat tgtccaggga gtcttgggcca ccatcaactt gcagtcaaca cagagctgc 840  
agctactgac caccctttctc ttcaacgtcc aggggactca gccaagatg gtgatggagt 900  
actggacggg gtggtttgac tcgtggggag gccctcacia tatcttggat tcttctgagg 960  
ttttgaaaac cgtgtctgcc attgtggacg ccggtcctc catcaacctc tacatgttcc 1020  
acggaggcac caactttggc ttcatgaatg gagccatgca cttccatgac tacaagtcag 1080  
atgtcaccag ctatgactat gatgctgtgc tgacagaagc cggcgattac acggccaagt 1140  
acatgaagct tcgagacttc ttcggtcca tctcaggcat ccctctccct ccccccactg 1200  
accttcttcc caagatgccg tatgagccct taacgccagt cttgtacctg tctctgtggg 1260  
acgcccctca gacctgggg gagccaatca agtctgaaaa gcccatcaac atggagaacc 1320  
tgccagtcaa tgggggaaat ggacagtcct tcgggtacat tctctatgag accagcatca 1380  
cctcgtctgg catcctcagt ggccacgtgc atgatcgggg gcagggtgtt gtgaacacag 1440  
tatccatagg attcttggac tacaagacaa cgaagattgc tgtccccctg atccagggtt 1500  
acaccgtgct gaggatcttg gtggagaatc gtgggcgagt caactatggg gagaatattg 1560  
atgaccagcg caaaggctta attggaaatc tctatctgaa tgattcacc ctgaaaaact 1620  
tcagaatcta tagcctggat atgaagaaga gcttctttca gaggttcggc ctggacaaat 1680  
ggngttccct ccagaaaca ccacattac ctgctttctt cttgggtagc ttgtccatca 1740  
gtccacgcgc ttgtgacacc tttctgaagc tggagggctg ggagaagggg gttgtattca 1800  
tcaatggcca gaaccttgga cgttactgga acattggacc ccagaagacg ctttacctcc 1860  
caggctccctg gttgagcagc ggaatcaacc aggtcatcgt ttttgaggag acgatggcgg 1920  
gccctgcatt acagttcacg gaaaccccc acctgggcag gaaccagtac attaatgtag 1980  
cgggtggacc cctcctgct ggtgccagtg ggagactgcc gcctcctctt gacctgaagc 2040  
ctggtggctg ctgccccacc cctcactgca aaagcatctc cttaagtagc aacctcaggg 2100  
actgggggct acagtctgcc cctgtctcag ctcaaaaccc taagcctgca gggaaagggtg 2160  
ggatggctct gggcctggct ttgttgatga tggctttcct acagccctgc tcttgtgccg 2220  
aggctgtcgg gctgtctcta ggggtgggag agctaatacag atcgcccagc ctttggccct 2280

cagaaaaagt gctgaaacgt gcccttgcac cggacgtcac agccctgcga gcattctgtg 2340  
 gactcaggcg tgctctttgc tggttcctgg gaggttggc cacatccctc atggcccat 2400  
 tttatccccg aaatcctggg tgtgtcacca gtgtagaggg tggggaaggg gtgtctcacc 2460  
 tgagctgact ttgttcttcc ttcacaacct tctgagcctt ctttgggatt ctggaaggaa 2520  
 ctcggcgtga gaaacatgtg acttcccctt tcccttccca ctcgctgctt cccacagggt 2580  
 gacaggctgg gctggagaaa cagaaatcct caccctgcgt cttcccaagt tagcagggtg 2640  
 ctctgggtgt cagtgaggag gacatgtgag tcctggcaga agccatggcc catgtctgca 2700  
 catccaggga ggaggacaga aggccagct cacatgtgag tcctggcaga agccatggcc 2760  
 catgtctgca catccaggga ggaggacaga aggccagct cacatgtgag tcctggcaga 2820  
 agccatggcc catgtctgca catccaggga ggaggacaga aggccagct cacatgtgag 2880  
 tcctggcaga agccatggcc catgtctgca catccaggga ggaggacaga aggccagct 2940  
 cagtggcccc cgctccccac cccccacgcc cgaacagcag gggcagagca gccctccttc 3000  
 gaagtgtgtc caagtccgca tttgagcctt gttctggggc ccagcccaac acctggcttg 3060  
 ggctcactgt cctgagttgc agtaaagcta taacctgaa tcacaa 3106

<210> 175

<211> 636

<212> PRT

<213> Homo sapiens

<220>

<221> MOD\_RES

<222> (539)

<223> Any amino acid

<400> 175

Met	Thr	Thr	Trp	Ser	Leu	Arg	Arg	Arg	Pro	Ala	Arg	Thr	Leu	Gly	Leu	1	5	10	15
Leu	Leu	Leu	Val	Val	Leu	Gly	Phe	Leu	Val	Leu	Arg	Arg	Leu	Asp	Trp	20	25	30	
Ser	Thr	Leu	Val	Pro	Leu	Arg	Leu	Arg	His	Arg	Gln	Leu	Gly	Leu	Gln	35	40	45	
Ala	Lys	Gly	Trp	Asn	Phe	Met	Leu	Glu	Asp	Ser	Thr	Phe	Trp	Ile	Phe	50	55	60	
Gly	Gly	Ser	Ile	His	Tyr	Phe	Arg	Val	Pro	Arg	Glu	Tyr	Trp	Arg	Asp	65	70	75	80
Arg	Leu	Leu	Lys	Met	Lys	Ala	Cys	Gly	Leu	Asn	Thr	Leu	Thr	Thr	Tyr	85	90	95	
Val	Pro	Trp	Asn	Leu	His	Glu	Pro	Glu	Arg	Gly	Lys	Phe	Asp	Phe	Ser	100	105	110	
Gly	Asn	Leu	Asp	Leu	Glu	Ala	Phe	Val	Leu	Met	Ala	Ala	Glu	Ile	Gly	115	120	125	
Leu	Trp	Val	Ile	Leu	Arg	Pro	Gly	Pro	Tyr	Ile	Cys	Ser	Glu	Met	Asp	130	135	140	

09909320-071801

Leu 145	Gly	Gly	Leu	Pro	Ser 150	Trp	Leu	Leu	Gln	Asp 155	Pro	Gly	Met	Arg	Leu 160
Arg	Thr	Thr	Tyr	Lys 165	Gly	Phe	Thr	Glu	Ala 170	Val	Asp	Leu	Tyr	Phe 175	Asp
His	Leu	Met	Ser 180	Arg	Val	Val	Pro	Leu 185	Gln	Tyr	Lys	Arg	Gly 190	Gly	Pro
Ile	Ile	Ala 195	Val	Gln	Val	Glu	Asn 200	Glu	Tyr	Gly	Ser	Tyr 205	Asn	Lys	Asp
Pro	Ala 210	Tyr	Met	Pro	Tyr	Val 215	Lys	Lys	Ala	Leu	Glu 220	Asp	Arg	Gly	Ile
Val 225	Glu	Leu	Leu	Leu	Thr 230	Ser	Asp	Asn	Lys	Asp 235	Gly	Leu	Ser	Lys	Gly 240
Ile	Val	Gln	Gly	Val 245	Leu	Ala	Thr	Ile	Asn 250	Leu	Gln	Ser	Thr	His 255	Glu
Leu	Gln	Leu	Leu 260	Thr	Thr	Phe	Leu	Phe 265	Asn	Val	Gln	Gly	Thr 270	Gln	Pro
Lys	Met 275	Val	Met	Glu	Tyr	Trp	Thr 280	Gly	Trp	Phe	Asp	Ser 285	Trp	Gly	Gly
Pro	His 290	Asn	Ile	Leu	Asp	Ser 295	Ser	Glu	Val	Leu	Lys 300	Thr	Val	Ser	Ala
Ile 305	Val	Asp	Ala	Gly	Ser 310	Ser	Ile	Asn	Leu	Tyr	Met 315	Phe	His	Gly	Gly 320
Thr	Asn	Phe	Gly	Phe 325	Met	Asn	Gly	Ala	Met 330	His	Phe	His	Asp	Tyr 335	Lys
Ser	Asp	Val	Thr 340	Ser	Tyr	Asp	Tyr	Asp 345	Ala	Val	Leu	Thr	Glu 350	Ala	Gly
Asp	Tyr 355	Thr	Ala	Lys	Tyr	Met	Lys 360	Leu	Arg	Asp	Phe	Phe 365	Gly	Ser	Ile
Ser	Gly 370	Ile	Pro	Leu	Pro	Pro 375	Pro	Pro	Asp	Leu	Leu 380	Pro	Lys	Met	Pro
Tyr 385	Glu	Pro	Leu	Thr	Pro 390	Val	Leu	Tyr	Leu	Ser 395	Leu	Trp	Asp	Ala	Leu 400
Lys	Tyr	Leu	Gly	Glu 405	Pro	Ile	Lys	Ser	Glu 410	Lys	Pro	Ile	Asn	Met 415	Glu
Asn	Leu	Pro	Val 420	Asn	Gly	Gly	Asn 425	Gly	Gln	Ser	Phe	Gly 430	Tyr	Ile	Leu

Tyr Glu Thr Ser Ile Thr Ser Ser Gly Ile Leu Ser Gly His Val His  
435 440 445

Asp Arg Gly Gln Val Phe Val Asn Thr Val Ser Ile Gly Phe Leu Asp  
450 455 460

Tyr Lys Thr Thr Lys Ile Ala Val Pro Leu Ile Gln Gly Tyr Thr Val  
465 470 475 480

Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly Glu Asn  
485 490 495

Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu Asn Asp  
500 505 510

Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys Lys Ser  
515 520 525

Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Xaa Ser Leu Pro Glu Thr  
530 535 540

Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser Ser Thr  
545 550 555 560

Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly Val Val  
565 570 575

Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly Pro Gln  
580 585 590

Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile Asn Gln  
595 600 605

Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln Phe Thr  
610 615 620

Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys  
625 630 635

<210> 176

<211> 2505

<212> DNA

<213> Homo sapiens

<400> 176

ggggacgcgg agctgagagg ctccgggcta gctaggtgta ggggtggacg ggtcccagga 60  
ccctggtgag ggttctctac ttggccttcg gtgggggtca agacgcaggc acctacgcca 120  
aaggggagca aagccgggct cggcccgagg cccccaggac ctccatctcc caatgttgga 180  
ggaatccgac acgtgacggg ctgtccgcgc tctcagacta gaggagcgct gtaaaccgcca 240  
tggctcccaa gaagctgtcc tgccttcgtt cctgctgct ggcgtcagc ctgacgctac 300  
tgctgcccc ggcagacact cggtcgttcg tagtggatag gggcatgac cggtttctcc 360  
tagacggggc cccgttcgcg tatgtgtctg gcagcctgca ctactttcgg gtaccgcggg 420



tgctttgggc cgaccggctt ttgaagatgc gatggagcgg cctcaacgcc atacagtttt 480  
 atgtgccctg gaactaccac gagccacagc ctgggggtcta taactttaat ggcagccggg 540  
 acctcattgc ctttctgaat gaggcagctc tagcgaacct gttggtcata ctgagaccag 600  
 gaccttacat ctgtgcagag tgggagatgg ggggtctccc atcctgggtg cttcgaaaac 660  
 ctgaaattca tctaagaacc tcagatccag acttccttgc cgcagtggac tcctggttca 720  
 aggtccttgc gcccaagata tatccatggc tttatcacia tgggggcaac atcattagca 780  
 ttcaggtgga gaatgaatat ggtagctaca gagcctgtga cttcagctac atgaggcact 840  
 tggctgggct cttccgtgca ctgctaggag aaaagatctt gctcttcacc acagatgggc 900  
 ctgaaggact caagtgtggc tccctccggg gactctatac cactgtagat tttggcccag 960  
 ctgacaacat gaccaaatac tttaccctgc ttcggaagta tgaaccccat gggccattgg 1020  
 taaactctga gtactacaca ggctggctgg attactgggg ccagaatcac tccacacggg 1080  
 ctgtgtcagc tgtaaccaa ggactagaga acatgctcaa gttgggagcc agtgtgaaca 1140  
 tgtacatgtt ccatggaggt accaactttg gatattggaa tgggtccgat aagaaggagc 1200  
 gcttccttcc gattactacc agctatgact atgatgcacc tatactctgaa gcaggggacc 1260  
 ccacaccta gcttttttgc cttcgagatg tcatcagcaa gttccaggaa gttccttttg 1320  
 gacctttacc tcccccgagc cccaagatga tgcttggacc tgtgactctg cacctgggtg 1380  
 ggcatttact ggcttttcta gacttgcttt gcccccggtg gcccatctat tcaatcttgc 1440  
 caatgacctt tgaggctgtc aagcaggacc atgggttcat gttgtaccga acctatatga 1500  
 cccataccat ttttgagcca acaccattct ggggtgcccc taatggagtc catgaccgtg 1560  
 cctatgtgat ggtggatggg gtgttccagg gtgttgtgga gcgaaatatg agagacaaac 1620  
 tatttttgac ggggaaactg ggggtccaaac tggatatctt ggtggagaac atggggaggc 1680  
 tcagcttttg gtctaacagc agtgacttca agggcctgtt gaagccacca attctggggc 1740  
 aaacaatcct taccagtggt atgatgttcc ctctgaaaat tgataacctt gtgaagtggg 1800  
 ggtttccctt ccagttgcca aaatggccat atcctcaagc tccttctggc cccacattct 1860  
 actccaaaac atttccaatt ttaggtctag ttggggacac atttctatat ctacctggat 1920  
 ggaccaaggg ccaagtctgg atcaatgggt ttaacttggg ccggtactgg acaaagcagg 1980  
 ggccacaaca gacctctac gtgccaagat tctgtctgtt tcttagggga gccctcaaca 2040  
 aaattacatt gctggaacta gaagatgtac ctctccagcc ccaagtccaa tttttggata 2100  
 agcctatcct caatagcact agtactttgc acaggacaca tatcaattcc ctttcagctg 2160  
 atacactgag tgccctctgaa ccaatggagt taagtgggca ctgaaaggta ggccgggcat 2220  
 ggtggctcat gcctgtaate ccagcacttt gggaggctga gacgggtgga ttacctgagg 2280  
 tcaggacttc aagaccagcc tggccaacat ggtgaaaccc cgtctccact aaaaatacaa 2340  
 aaattagccg ggcgtgatgg tgggcacctc taatcccagc tacttgggag gctgagggca 2400  
 ggagaattgc ttgaatccag gaggcagagg ttgcagttag tggaggttgt accactgcac 2460  
 tccagcctgg ctgacagtga gacactccat ctcaaaaaaa aaaaa 2505

<210> 177

<211> 654

<212> PRT

<213> Homo sapiens

<400> 177

Met Ala Pro Lys Lys Leu Ser Cys Leu Arg Ser Leu Leu Leu Pro Leu  
 1 5 10 15

Ser Leu Thr Leu Leu Leu Pro Gln Ala Asp Thr Arg Ser Phe Val Val  
 20 25 30

Asp Arg Gly His Asp Arg Phe Leu Leu Asp Gly Ala Pro Phe Arg Tyr  
 35 40 45

Val Ser Gly Ser Leu His Tyr Phe Arg Val Pro Arg Val Leu Trp Ala  
 50 55 60

Asp Arg Leu Leu Lys Met Arg Trp Ser Gly Leu Asn Ala Ile Gln Phe  
 65 70 75 80  
 Tyr Val Pro Trp Asn Tyr His Glu Pro Gln Pro Gly Val Tyr Asn Phe  
 85 90 95  
 Asn Gly Ser Arg Asp Leu Ile Ala Phe Leu Asn Glu Ala Ala Leu Ala  
 100 105 110  
 Asn Leu Leu Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ala Glu Trp  
 115 120 125  
 Glu Met Gly Gly Leu Pro Ser Trp Leu Leu Arg Lys Pro Glu Ile His  
 130 135 140  
 Leu Arg Thr Ser Asp Pro Asp Phe Leu Ala Ala Val Asp Ser Trp Phe  
 145 150 155 160  
 Lys Val Leu Leu Pro Lys Ile Tyr Pro Trp Leu Tyr His Asn Gly Gly  
 165 170 175  
 Asn Ile Ile Ser Ile Gln Val Glu Asn Glu Tyr Gly Ser Tyr Arg Ala  
 180 185 190  
 Cys Asp Phe Ser Tyr Met Arg His Leu Ala Gly Leu Phe Arg Ala Leu  
 195 200 205  
 Leu Gly Glu Lys Ile Leu Leu Phe Thr Thr Asp Gly Pro Glu Gly Leu  
 210 215 220  
 Lys Cys Gly Ser Leu Arg Gly Leu Tyr Thr Thr Val Asp Phe Gly Pro  
 225 230 235 240  
 Ala Asp Asn Met Thr Lys Ile Phe Thr Leu Leu Arg Lys Tyr Glu Pro  
 245 250 255  
 His Gly Pro Leu Val Asn Ser Glu Tyr Tyr Thr Gly Trp Leu Asp Tyr  
 260 265 270  
 Trp Gly Gln Asn His Ser Thr Arg Ser Val Ser Ala Val Thr Lys Gly  
 275 280 285  
 Leu Glu Asn Met Leu Lys Leu Gly Ala Ser Val Asn Met Tyr Met Phe  
 290 295 300  
 His Gly Gly Thr Asn Phe Gly Tyr Trp Asn Gly Ala Asp Lys Lys Gly  
 305 310 315 320  
 Arg Phe Leu Pro Ile Thr Thr Ser Tyr Asp Tyr Asp Ala Pro Ile Ser  
 325 330 335  
 Glu Ala Gly Asp Pro Thr Pro Lys Leu Phe Ala Leu Arg Asp Val Ile

FOBT20"02E60660

	340		345		350
Ser Lys Phe Gln Glu Val Pro Leu Gly Pro Leu Pro Pro Pro Ser Pro	355		360		365
Lys Met Met Leu Gly Pro Val Thr Leu His Leu Val Gly His Leu Leu	370		375		380
Ala Phe Leu Asp Leu Leu Cys Pro Arg Gly Pro Ile His Ser Ile Leu	385		390		395
Pro Met Thr Phe Glu Ala Val Lys Gln Asp His Gly Phe Met Leu Tyr		405		410	415
Arg Thr Tyr Met Thr His Thr Ile Phe Glu Pro Thr Pro Phe Trp Val		420		425	430
Pro Asn Asn Gly Val His Asp Arg Ala Tyr Val Met Val Asp Gly Val		435		440	445
Phe Gln Gly Val Val Glu Arg Asn Met Arg Asp Lys Leu Phe Leu Thr		450		455	460
Gly Lys Leu Gly Ser Lys Leu Asp Ile Leu Val Glu Asn Met Gly Arg		465		470	475
Leu Ser Phe Gly Ser Asn Ser Ser Asp Phe Lys Gly Leu Leu Lys Pro		485		490	495
Pro Ile Leu Gly Gln Thr Ile Leu Thr Gln Trp Met Met Phe Pro Leu		500		505	510
Lys Ile Asp Asn Leu Val Lys Trp Trp Phe Pro Leu Gln Leu Pro Lys		515		520	525
Trp Pro Tyr Pro Gln Ala Pro Ser Gly Pro Thr Phe Tyr Ser Lys Thr		530		535	540
Phe Pro Ile Leu Gly Ser Val Gly Asp Thr Phe Leu Tyr Leu Pro Gly		545		550	555
Trp Thr Lys Gly Gln Val Trp Ile Asn Gly Phe Asn Leu Gly Arg Tyr		565		570	575
Trp Thr Lys Gln Gly Pro Gln Gln Thr Leu Tyr Val Pro Arg Phe Leu		580		585	590
Leu Phe Pro Arg Gly Ala Leu Asn Lys Ile Thr Leu Leu Glu Leu Glu		595		600	605
Asp Val Pro Leu Gln Pro Gln Val Gln Phe Leu Asp Lys Pro Ile Leu		610		615	620

09909320-071801

Asn Ser Thr Ser Thr Leu His Arg Thr His Ile Asn Ser Leu Ser Ala  
625 630 635 640

Asp Thr Leu Ser Ala Ser Glu Pro Met Glu Leu Ser Gly His  
645 650

<210> 178

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 178

tggctactcc aagaccctgg catg

24

<210> 179

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 179

tggacaaatc cccttgctca gccc

24

<210> 180

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 180

gggcttcacc gaagcagtgg acctttatatt tgaccacctg atgtccaggg

50

<210> 181

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 181

ccagctatga ctatgatgca cc

22

00909320.071001

<210> 182  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 182  
 tggcaccag aatggtgttg gctc 24

<210> 183  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 183  
 cgagatgtca tcagcaagtt ccaggaagtt cctttgggac ctttacctcc 50

<210> 184  
 <211> 1947  
 <212> DNA  
 <213> Homo sapiens

<400> 184  
 gctttgaaca cgtctgcaag cccaaagttg agcatctgat tggttatgag gtatttgagt 60  
 gcaccacaa tatggcttac atgttgaaaa agcttctcat cagttacata tccattattt 120  
 gtggttatgg ctttatctgc ctctacactc tcttctgggt attcaggata cctttgaagg 180  
 aatattcttt cgaaaaagtc agagaagaga gcagtttttag tgacattcca gatgtcaaaa 240  
 acgattttgc gttccttctt cacatggtag accagtatga ccagctatat tccaagcggt 300  
 ttggtgtgtt cttgtcagaa gttagtgaata ataaacttag ggaaattagt ttgaaccatg 360  
 agtggacatt tgaaaaactc aggcagcaca ttacacgcaa cgcccaggac aagcaggagt 420  
 tgcattctgt catgctgtcg ggggtgcccg atgctgtctt tgacctcaca gacctggatg 480  
 tgctaaagct tgaactaatt ccagaagcta aaattcctgc taagatttct caaatgacta 540  
 acctccaaga gctccacctc tgccactgcc ctgcaaaagt tgaacagact gcttttagct 600  
 ttcttcgcga tcaattgaga tgccctcacg tgaagttcac tgatgtggct gaaattcctg 660  
 cctgggtgta tttgctcaaa aaccttcgag agttgtactt aataggcaat ttgaactctg 720  
 aaaacaataa gatgatagga cttgaatctc tccgagagtt gcggcacctt aagattctcc 780  
 acgtgaagag caatttgacc aaagttccct ccaacattac agatgtggct ccacatctta 840  
 caaagttagt cattcataat gacggcacta aactcttggt actgaacagc ctttaagaaa 900  
 tgatgaatgt cgctgagctg gaactccaga actgtgagct agagagaatc ccacatgcta 960  
 ttttcagcct ctctaattta caggaaactgg atttaaagtc caataacatt cgcacaattg 1020  
 aggaaatcat cagtttccag catttaaaac gactgacttg tttaaaatta tggcataaca 1080  
 aaattgttac tattcctccc tctattacce atgtcaaaaa cttggagtca ctttatttct 1140  
 ctaacaacaa gctcgaatcc ttaccagtgg cagtatttag tttacagaaa ctcagatgct 1200  
 tagatgtgag ctacaacaac atttcaatga ttccaataga aataggattg cttcagaacc 1260  
 tgcagcattt gcatatcact gggaacaaag tggacattct gccaaaacaa ttgtttaaat 1320

gcataaagtt gaggactttg aatctgggac agaactgcat cacctcactc ccagagaaaag 1380  
 ttggtcagct ctcccagctc actcagctgg agctgaaggg gaactgcttg gaccgcctgc 1440  
 cagcccagct gggccagtgt cggatgctca agaaaagcgg gcttggttg gaagatcacc 1500  
 tttttgatac cctgccactc gaagtcaaag aggcattgaa tcaagacata aatattccct 1560  
 ttgcaaattg gatttaaact aagataatat atgcacagtg atgtgcagga acaacttcct 1620  
 agattgcaag tgctcacgta caagttatta caagataatg catttttagga gtagatacat 1680  
 cttttaaaat aaaacagaga ggatgcatag aaggctgata gaagacataa ctgaatgttc 1740  
 aatgtttgta gggttttaag tcattcattt ccaaatacatt tttttttttc ttttggggaa 1800  
 agggaaggaa aaattataat cactaatctt gggtcttttt aaattgtttg taacttggat 1860  
 gctgccgcta ctgaatgttt acaaattgct tgcttgctaa agtaaataat taaattgaca 1920  
 ttttcttact aaaaaaaaaa aaaaaaa 1947

<210> 185

<211> 501

<212> PRT

<213> Homo sapiens

<400> 185

Met Ala Tyr Met Leu Lys Lys Leu Leu Ile Ser Tyr Ile Ser Ile Ile  
 1 5 10 15

Cys Val Tyr Gly Phe Ile Cys Leu Tyr Thr Leu Phe Trp Leu Phe Arg  
 20 25 30

Ile Pro Leu Lys Glu Tyr Ser Phe Glu Lys Val Arg Glu Glu Ser Ser  
 35 40 45

Phe Ser Asp Ile Pro Asp Val Lys Asn Asp Phe Ala Phe Leu Leu His  
 50 55 60

Met Val Asp Gln Tyr Asp Gln Leu Tyr Ser Lys Arg Phe Gly Val Phe  
 65 70 75 80

Leu Ser Glu Val Ser Glu Asn Lys Leu Arg Glu Ile Ser Leu Asn His  
 85 90 95

Glu Trp Thr Phe Glu Lys Leu Arg Gln His Ile Ser Arg Asn Ala Gln  
 100 105 110

Asp Lys Gln Glu Leu His Leu Phe Met Leu Ser Gly Val Pro Asp Ala  
 115 120 125

Val Phe Asp Leu Thr Asp Leu Asp Val Leu Lys Leu Glu Leu Ile Pro  
 130 135 140

Glu Ala Lys Ile Pro Ala Lys Ile Ser Gln Met Thr Asn Leu Gln Glu  
 145 150 155 160

Leu His Leu Cys His Cys Pro Ala Lys Val Glu Gln Thr Ala Phe Ser  
 165 170 175

Phe Leu Arg Asp His Leu Arg Cys Leu His Val Lys Phe Thr Asp Val  
 180 185 190

09909320.071801

Ala	Glu	Ile	Pro	Ala	Trp	Val	Tyr	Leu	Leu	Lys	Asn	Leu	Arg	Glu	Leu
195						200						205			
Tyr	Leu	Ile	Gly	Asn	Leu	Asn	Ser	Glu	Asn	Asn	Lys	Met	Ile	Gly	Leu
210						215						220			
Glu	Ser	Leu	Arg	Glu	Leu	Arg	His	Leu	Lys	Ile	Leu	His	Val	Lys	Ser
225						230						235			
Asn	Leu	Thr	Lys	Val	Pro	Ser	Asn	Ile	Thr	Asp	Val	Ala	Pro	His	Leu
			245						250			255			
Thr	Lys	Leu	Val	Ile	His	Asn	Asp	Gly	Thr	Lys	Leu	Leu	Val	Leu	Asn
			260						265			270			
Ser	Leu	Lys	Lys	Met	Met	Asn	Val	Ala	Glu	Leu	Glu	Leu	Gln	Asn	Cys
275						280						285			
Glu	Leu	Glu	Arg	Ile	Pro	His	Ala	Ile	Phe	Ser	Leu	Ser	Asn	Leu	Gln
290						295						300			
Glu	Leu	Asp	Leu	Lys	Ser	Asn	Asn	Ile	Arg	Thr	Ile	Glu	Glu	Ile	Ile
305						310						315			
Ser	Phe	Gln	His	Leu	Lys	Arg	Leu	Thr	Cys	Leu	Lys	Leu	Trp	His	Asn
			325						330			335			
Lys	Ile	Val	Thr	Ile	Pro	Pro	Ser	Ile	Thr	His	Val	Lys	Asn	Leu	Glu
			340						345			350			
Ser	Leu	Tyr	Phe	Ser	Asn	Asn	Lys	Leu	Glu	Ser	Leu	Pro	Val	Ala	Val
355						360						365			
Phe	Ser	Leu	Gln	Lys	Leu	Arg	Cys	Leu	Asp	Val	Ser	Tyr	Asn	Asn	Ile
370						375						380			
Ser	Met	Ile	Pro	Ile	Glu	Ile	Gly	Leu	Leu	Gln	Asn	Leu	Gln	His	Leu
385						390						395			
His	Ile	Thr	Gly	Asn	Lys	Val	Asp	Ile	Leu	Pro	Lys	Gln	Leu	Phe	Lys
			405						410			415			
Cys	Ile	Lys	Leu	Arg	Thr	Leu	Asn	Leu	Gly	Gln	Asn	Cys	Ile	Thr	Ser
			420						425			430			
Leu	Pro	Glu	Lys	Val	Gly	Gln	Leu	Ser	Gln	Leu	Thr	Gln	Leu	Glu	Leu
435						440						445			
Lys	Gly	Asn	Cys	Leu	Asp	Arg	Leu	Pro	Ala	Gln	Leu	Gly	Gln	Cys	Arg
450						455						460			
Met	Leu	Lys	Lys	Ser	Gly	Leu	Val	Val	Glu	Asp	His	Leu	Phe	Asp	Thr

<400> 189  
 cccacgcgctc cggcctttctc tctggacttt gcattttccat tcctttttcat tgacaaaactg 60  
 actttttttta tttcttttttt tccatctctg ggccagcttg ggatcctagg ccgccctggg 120  
 aagacatttg tgttttacac acataaggat ctgtgttttg ggtttcttct tcctcccttg 180



acattggcat tgcttagtgg ttgtgtgggg agggagacca cgtgggctca gtgcttgctt 240  
 gcacttatct gcctaggtac atcgaagtct tttgacctcc atacagtgat tatgcctgtc 300  
 atcgctggtg gtatcctggc ggccttgctc ctgctgatag ttgtcgtgct ctgtctttac 360  
 ttcaaaatac acaacgcgct aaaagctgca aaggaaacctg aagctgtggc tgtaaaaaat 420  
 cacaaccag acaaggtgtg gtgggccaag aacagccagg ccaaaaccat tgccacggag 480  
 tcttgctctg ccctgcagtg ctgtgaagga tatagaatgt gtgccagttt tgattccctg 540  
 ccaccttgct gttgcgacat aaatgagggc ctctgagtta ggaaaggctc ccttctcaaa 600  
 gcagagccct gaagacttca atgatgtcaa tgaggccacc tgtttgtgat gtgcaggcac 660  
 agaagaaagg cacagctccc catcagtttc atggaaaata actcagtgcc tgctgggaac 720  
 cagctgctgg agatccctac agagagcttc cactgggggc aaccttcca ggaaggagt 780  
 ggggagagag aacctcact gtggggaatg ctgataaacc agtcacacag ctgctctatt 840  
 ctcacacaaa tctacctctt gcgtggctgg aactgacgtt tccttgaggg tgtccagaaa 900  
 gctgatgtaa cacagagcct ataaaagctg tcggtcctta aggctgcccc gcgccttgcc 960  
 aaaatggagc ttgtaagaag gctcatgcca ttgacctctc taattctctc ctgtttgggc 1020  
 gagctgacaa tggcggaggc tgaaggcaat gcaagctgca cagtcagtct aggggggtgcc 1080  
 aatatggcag agaccacaaa agccatgatc ctgcaactca atcccagtga gaactgcacc 1140  
 tggacaatag aaagaccaga aaacaaaagc atcagaatta tcttttctta tgtccagctt 1200  
 gatccagatg gaagctgtga aagtgaaaac attaaagtct ttgacggaac ctccagcaat 1260  
 gggcctctgc tagggcaagt ctgcagtaaa aacgactatg ttctgtatt tgaatcatca 1320  
 tccagtacat tgacgtttca aatagttact gactcagcaa gaattcaaag aactgtcttt 1380  
 gtcttctact acttcttctc tctaaccatc tctattccaa actgtggcgg ttacctggat 1440  
 accttggagc gatccttcac cagccccaat taccacaaagc cgcacctga gctggcttat 1500  
 tgtgtgtggc acatacaagt ggagaaagat tacaagataa aactaaactt caaagagatt 1560  
 ttctagaaa tagacaaaca gtgcaaat tttgatttcttg ccatctatga tggccccctc 1620  
 accaactctg gcctgattgg acaagtctgt ggccgtgtga ctcccacctt cgaatcgtca 1680  
 tcaaactctc tgactgtcgt gttgtctaca gattatgcca attcttaccg gggattttct 1740  
 gcttcttaca cctcaattta tgcagaaaac atcaacacta catctttaac ttgtcttct 1800  
 gacaggatga gagttattat aagcaaatcc tacctagagg cttttaactc taatgggaat 1860  
 aacttgcaac taaaagacc aacttgacga ccaaaattat caaatgttgt ggaattttct 1920  
 gtccctctta atggatgtgg tacaatcaga aaggtagaag atcagtcaat tacttacacc 1980  
 aatataatca ccttttctgc atcctcaact tctgaagtga tccccgtca gaaacaactc 2040  
 cagattattg tgaagtgtga aatgggacat aattctacag tggagataat atacataaca 2100  
 gaagatgatg taatacaaaag tcaaaatgca ctgggcaaat ataacaccag catggctctt 2160  
 tttgaatcca attcatttga aaagactata cttgaatcac catattatgt ggatttgaac 2220  
 caaactctt ttgttcaagt tagtctgcac acctcagatc caaatttggg ggtgtttctt 2280  
 gatccctgta gagcctctcc cacctctgac tttgcatctc caacctacga cctaatacaag 2340  
 agtggatgta gtcgagatga aacttgtaag gtgtatccct tatttggaca ctatgggaga 2400  
 ttccagttta atgcctttaa attcttgaga agtatgagct ctgtgtatct gcagtgtaaa 2460  
 gttttgatat gtgatagcag tgaccaccag tctcgtgca atcaagggtg tgtctccaga 2520  
 agcaaacgag acatttcttc atataaatgg aaaacagatt ccatcatagg acccattcgt 2580  
 ctgaaaagg atcgaagtgc aagtggcaat tcaggatttc agcatgaaac acatgcggaa 2640  
 gaaactccaa accagccttt caacagtgtg catctgtttt ccttcattgg tctagctctg 2700  
 aatgtggtga ctgtagcgac aatcacagtg aggcattttg taaatcaacg ggcagactac 2760  
 aaataccaga agctgcagaa ctattaacta acaggtccaa ccctaagtga gacatgttc 2820  
 tccaggatgc caaaggaaat gctacctcgt ggctacacat attatgaata aatgaggaag 2880  
 ggcctgaaag tgacacacag gcctgcatgt aaaaaaa 2917

<210> 190

<211> 607

<212> PRT

<213> Homo sapiens

<400> 190

Met	Glu	Leu	Val	Arg	Arg	Leu	Met	Pro	Leu	Thr	Leu	Leu	Ile	Leu	Ser	1	5	10	15
Cys	Leu	Ala	Glu	Leu	Thr	Met	Ala	Glu	Ala	Glu	Gly	Asn	Ala	Ser	Cys	20	25	30	
Thr	Val	Ser	Leu	Gly	Gly	Ala	Asn	Met	Ala	Glu	Thr	His	Lys	Ala	Met	35	40	45	
Ile	Leu	Gln	Leu	Asn	Pro	Ser	Glu	Asn	Cys	Thr	Trp	Thr	Ile	Glu	Arg	50	55	60	
Pro	Glu	Asn	Lys	Ser	Ile	Arg	Ile	Ile	Phe	Ser	Tyr	Val	Gln	Leu	Asp	65	70	75	80
Pro	Asp	Gly	Ser	Cys	Glu	Ser	Glu	Asn	Ile	Lys	Val	Phe	Asp	Gly	Thr	85	90	95	
Ser	Ser	Asn	Gly	Pro	Leu	Leu	Gly	Gln	Val	Cys	Ser	Lys	Asn	Asp	Tyr	100	105	110	
Val	Pro	Val	Phe	Glu	Ser	Ser	Ser	Ser	Thr	Leu	Thr	Phe	Gln	Ile	Val	115	120	125	
Thr	Asp	Ser	Ala	Arg	Ile	Gln	Arg	Thr	Val	Phe	Val	Phe	Tyr	Tyr	Phe	130	135	140	
Phe	Ser	Pro	Asn	Ile	Ser	Ile	Pro	Asn	Cys	Gly	Gly	Tyr	Leu	Asp	Thr	145	150	155	160
Leu	Glu	Gly	Ser	Phe	Thr	Ser	Pro	Asn	Tyr	Pro	Lys	Pro	His	Pro	Glu	165	170	175	
Leu	Ala	Tyr	Cys	Val	Trp	His	Ile	Gln	Val	Glu	Lys	Asp	Tyr	Lys	Ile	180	185	190	
Lys	Leu	Asn	Phe	Lys	Glu	Ile	Phe	Leu	Glu	Ile	Asp	Lys	Gln	Cys	Lys	195	200	205	
Phe	Asp	Phe	Leu	Ala	Ile	Tyr	Asp	Gly	Pro	Ser	Thr	Asn	Ser	Gly	Leu	210	215	220	
Ile	Gly	Gln	Val	Cys	Gly	Arg	Val	Thr	Pro	Thr	Phe	Glu	Ser	Ser	Ser	225	230	235	240
Asn	Ser	Leu	Thr	Val	Val	Leu	Ser	Thr	Asp	Tyr	Ala	Asn	Ser	Tyr	Arg	245	250	255	
Gly	Phe	Ser	Ala	Ser	Tyr	Thr	Ser	Ile	Tyr	Ala	Glu	Asn	Ile	Asn	Thr	260	265	270	
Thr	Ser	Leu	Thr	Cys	Ser	Ser	Asp	Arg	Met	Arg	Val	Ile	Ile	Ser	Lys	275	280	285	

09909320-071801

Ser Tyr Leu Glu Ala Phe Asn Ser Asn Gly Asn Asn Leu Gln Leu Lys  
 290 295 300  
 Asp Pro Thr Cys Arg Pro Lys Leu Ser Asn Val Val Glu Phe Ser Val  
 305 310 315 320  
 Pro Leu Asn Gly Cys Gly Thr Ile Arg Lys Val Glu Asp Gln Ser Ile  
 325 330 335  
 Thr Tyr Thr Asn Ile Ile Thr Phe Ser Ala Ser Ser Thr Ser Glu Val  
 340 345 350  
 Ile Thr Arg Gln Lys Gln Leu Gln Ile Ile Val Lys Cys Glu Met Gly  
 355 360 365  
 His Asn Ser Thr Val Glu Ile Ile Tyr Ile Thr Glu Asp Asp Val Ile  
 370 375 380  
 Gln Ser Gln Asn Ala Leu Gly Lys Tyr Asn Thr Ser Met Ala Leu Phe  
 385 390 395 400  
 Glu Ser Asn Ser Phe Glu Lys Thr Ile Leu Glu Ser Pro Tyr Tyr Val  
 405 410 415  
 Asp Leu Asn Gln Thr Leu Phe Val Gln Val Ser Leu His Thr Ser Asp  
 420 425 430  
 Pro Asn Leu Val Val Phe Leu Asp Thr Cys Arg Ala Ser Pro Thr Ser  
 435 440 445  
 Asp Phe Ala Ser Pro Thr Tyr Asp Leu Ile Lys Ser Gly Cys Ser Arg  
 450 455 460  
 Asp Glu Thr Cys Lys Val Tyr Pro Leu Phe Gly His Tyr Gly Arg Phe  
 465 470 475 480  
 Gln Phe Asn Ala Phe Lys Phe Leu Arg Ser Met Ser Ser Val Tyr Leu  
 485 490 495  
 Gln Cys Lys Val Leu Ile Cys Asp Ser Ser Asp His Gln Ser Arg Cys  
 500 505 510  
 Asn Gln Gly Cys Val Ser Arg Ser Lys Arg Asp Ile Ser Ser Tyr Lys  
 515 520 525  
 Trp Lys Thr Asp Ser Ile Ile Gly Pro Ile Arg Leu Lys Arg Asp Arg  
 530 535 540  
 Ser Ala Ser Gly Asn Ser Gly Phe Gln His Glu Thr His Ala Glu Glu  
 545 550 555 560  
 Thr Pro Asn Gln Pro Phe Asn Ser Val His Leu Phe Ser Phe Met Val

0909320.071804  
 108720.02E60650

	565		570		575										
Leu	Ala	Leu	Asn	Val	Val	Thr	Val	Ala	Thr	Ile	Thr	Val	Arg	His	Phe
		580						585					590		
Val	Asn	Gln	Arg	Ala	Asp	Tyr	Lys	Tyr	Gln	Lys	Leu	Gln	Asn	Tyr	
	595						600					605			

<210> 191  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 191  
 tctctattcc aaactgtggc g 21

<210> 192  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 192  
 tttgatgacg attcgaaggt gg 22

<210> 193  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 193  
 ggaaggatcc ttcaccagcc ccaattaccc aaagccgcat cctgagc 47

<210> 194  
 <211> 2362  
 <212> DNA  
 <213> Homo sapiens

<400> 194  
 gacggaagaa cagcgctccc gaggccgcgg gagcctgcag agaggacagc cggcctgcgc 60  
 cgggacatgc ggccccagga gctccccagg ctgcgcgttcc cggtgctgct gttgctgttg 120  
 ctgctgctgc cgccgcgcgc gtgccctgcc cacagcgcca cgcgcttcga cccacactgg 180

FOBT20"02E60660

gagtccttgg acgcccgcga gctgcccgcg tggtttgacc aggccaaagt cggcatcttc 240  
 atccactggg gagtggtttc cgtgcccagc ttcggtagcg agtggttctg gtggtattgg 300  
 caaaaggaaa agataccgaa gtatgtggaa tttatgaaag ataattaccc tcctagtttc 360  
 aaatatgaag attttggacc actatttaca gcaaaatttt ttaatgccaa ccagtgggca 420  
 gatatttttc aggcctctgg tgccaaatac attgtcttaa ctccaaaca tcatgaaggc 480  
 tttaccttgt ggggggtcaga atattcgtgg aactggaatg ccatagatga ggggcccag 540  
 agggacattg tcaaggaaact tgaggtagcc attaggaaca gaactgacct gcgttttgga 600  
 ctgtactatt ccctttttga atggtttcat ccgctcttcc ttgaggatga atccagttca 660  
 ttccataagc ggcaatttcc agtttctaag acattgccag agctctatga gttagtgaac 720  
 aactatcagc ctgaggttct gtggtcggat ggtgacggag gagcacggga tcaatactgg 780  
 aacagcacag gcttcttggc ctggttatat aatgaaagcc cagttcgggg cacagtagtc 840  
 accaatgatc gttggggagc tggtagcatc tgtaagcatg gtggcttcta tacctgcagt 900  
 gatcggtata acccaggaca tcttttgcca cataaatggg aaaactgcat gacaatagac 960  
 aaactgtcct ggggctatag gagggaagct ggaatctctg actatcttac aattgaagaa 1020  
 ttggtgaagc aacttgtaga gacagtttca tgtggaggaa atcttttgat gaattattggg 1080  
 cccacactag atggcaccat ttctgtagtt tttgaggagc gactgaggca agtgggggtcc 1140  
 tggctaaaag tcaatggaga agctatttat gaaacctata cctggcgatc ccagaatgac 1200  
 actgtcacc cagatgtgtg gtacacatcc aagcctaaag aaaaattagt ctatgccatt 1260  
 tttcttaaat ggcccacatc aggacagctg ttccttggcc atcccaaagc tattctgggg 1320  
 gcaacagagg tgaaactact gggccatgga cagccactta actggatttc tttggagcaa 1380  
 aatggcatta tggtagaact gccacagcta accattcatc agatgccgtg taaatggggc 1440  
 tgggctctag ccctaactaa tgtgatctaa agtgcagcag agtggctgat gctgcaagtt 1500  
 atgtctaagg ctaggaacta tcaggtgtct ataattgtag cacatggaga aagcaatgta 1560  
 aactggataa gaaaattatt tggcagttca gccctttccc tttttcccac taaatttttc 1620  
 ttaattacc catgtaacca ttttaactct ccagtgcact ttgccattaa agtctcttca 1680  
 cattgatttg tttccatgtg tgactcagag gtgagaattt tttcacatta tagtagcaag 1740  
 gaattgggtg tattatggac cgaactgaaa attttatgtt gaagccatat ccccatgat 1800  
 tatatagtta tgcactactt aatatgggga tattttctgg gaaatgcatt gctagtcaat 1860  
 ttttttttgt gccaacatca tagagtgtat ttacaaaatc ctatagggca tagcctacta 1920  
 cacaccta atgtgatggta tagactgttg ctctaggct acagacatat acagcatgtt 1980  
 actgaatact gtaggcaata gtaacagtgg tatttgtata tcgaaacata tggaaacata 2040  
 gagaaggtag agtaaaaata ctgtaaaata aatggtgcac ctgtataggg cacttaccac 2100  
 gaatggagct tacaggactg gaagttgctc tgggtgagtc agtgagtga tgtgaaggcc 2160  
 taggacatta ttgaacactg ccagacgtta taaatactgt atgcttaggc tacactacat 2220  
 ttataaaaaa aagtttttct ttcttcaatt ataaattaac ataagtgtac tgaacttta 2280  
 caaacgtttt aattttttaa acctttttgg ctcttttgta ataactta gcttaaaaca 2340  
 taaactcatt gtgcaaatgt aa 2362

<210> 195

<211> 467

<212> PRT

<213> Homo sapiens

<400> 195

Met Arg Pro Gln Glu Leu Pro Arg Leu Ala Phe Pro Leu Leu Leu Leu  
 1 5 10 15

Leu Leu Leu Leu Leu Pro Pro Pro Pro Cys Pro Ala His Ser Ala Thr  
 20 25 30

Arg Phe Asp Pro Thr Trp Glu Ser Leu Asp Ala Arg Gln Leu Pro Ala  
 35 40 45

Trp	Phe 50	Asp	Gln	Ala	Lys	Phe 55	Gly	Ile	Phe	Ile	His 60	Trp	Gly	Val	Phe
Ser 65	Val	Pro	Ser	Phe	Gly 70	Ser	Glu	Trp	Phe	Trp 75	Trp	Tyr	Trp	Gln	Lys 80
Glu	Lys	Ile	Pro	Lys 85	Tyr	Val	Glu	Phe	Met 90	Lys	Asp	Asn	Tyr	Pro 95	Pro
Ser	Phe	Lys	Tyr 100	Glu	Asp	Phe	Gly	Pro 105	Leu	Phe	Thr	Ala	Lys 110	Phe	Phe
Asn	Ala	Asn 115	Gln	Trp	Ala	Asp	Ile 120	Phe	Gln	Ala	Ser	Gly 125	Ala	Lys	Tyr
Ile 130	Val	Leu	Thr	Ser	Lys	His 135	His	Glu	Gly	Phe	Thr 140	Leu	Trp	Gly	Ser
Glu 145	Tyr	Ser	Trp	Asn	Trp 150	Asn	Ala	Ile	Asp	Glu	Gly 155	Pro	Lys	Arg	Asp 160
Ile	Val	Lys	Glu	Leu 165	Glu	Val	Ala	Ile	Arg 170	Asn	Arg	Thr	Asp	Leu 175	Arg
Phe	Gly	Leu 180	Tyr	Tyr	Ser	Leu	Phe	Glu 185	Trp	Phe	His	Pro	Leu 190	Phe	Leu
Glu	Asp	Glu 195	Ser	Ser	Ser	Phe	His 200	Lys	Arg	Gln	Phe	Pro	Val	Ser	Lys
Thr 210	Leu	Pro	Glu	Leu	Tyr	Glu 215	Leu	Val	Asn	Asn	Tyr 220	Gln	Pro	Glu	Val
Leu 225	Trp	Ser	Asp	Gly	Asp 230	Gly	Gly	Ala	Pro	Asp 235	Gln	Tyr	Trp	Asn	Ser 240
Thr	Gly	Phe	Leu 245	Ala	Trp	Leu	Tyr	Asn	Glu 250	Ser	Pro	Val	Arg	Gly 255	Thr
Val	Val	Thr 260	Asn	Asp	Arg	Trp	Gly	Ala 265	Gly	Ser	Ile	Cys	Lys 270	His	Gly
Gly	Phe	Tyr 275	Thr	Cys	Ser	Asp	Arg 280	Tyr	Asn	Pro	Gly	His 285	Leu	Leu	Pro
His 290	Lys	Trp	Glu	Asn	Cys	Met 295	Thr	Ile	Asp	Lys	Leu 300	Ser	Trp	Gly	Tyr
Arg 305	Arg	Glu	Ala	Gly	Ile 310	Ser	Asp	Tyr	Leu	Thr 315	Ile	Glu	Glu	Leu	Val 320
Lys	Gln	Leu	Val	Glu 325	Thr	Val	Ser	Cys	Gly 330	Gly	Asn	Leu	Leu	Met 335	Asn

Ile Gly Pro Thr Leu Asp Gly Thr Ile Ser Val Val Phe Glu Glu Arg  
                   340                                  345                                  350

Leu Arg Gln Val Gly Ser Trp Leu Lys Val Asn Gly Glu Ala Ile Tyr  
                   355                                  360                                  365

Glu Thr Tyr Thr Trp Arg Ser Gln Asn Asp Thr Val Thr Pro Asp Val  
                   370                                  375                                  380

Trp Tyr Thr Ser Lys Pro Lys Glu Lys Leu Val Tyr Ala Ile Phe Leu  
                   385                                  390                                  395                                  400

Lys Trp Pro Thr Ser Gly Gln Leu Phe Leu Gly His Pro Lys Ala Ile  
                                   405                                  410                                  415

Leu Gly Ala Thr Glu Val Lys Leu Leu Gly His Gly Gln Pro Leu Asn  
                   420                                  425                                  430

Trp Ile Ser Leu Glu Gln Asn Gly Ile Met Val Glu Leu Pro Gln Leu  
                   435                                  440                                  445

Thr Ile His Gln Met Pro Cys Lys Trp Gly Trp Ala Leu Ala Leu Thr  
                   450                                  455                                  460

Asn Val Ile  
 465

<210> 196

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 196

tggtttgacc aggccaagtt cgg

23

<210> 197

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 197

ggattcatcc tcaaggaaga gcgg

24

<210> 198

09909320-071801

<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 198  
 aacttcgcagc atcagccact ctgc 24

<210> 199  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 199  
 ttccgtgccc agcttcggta gcgagtgggt ctggtgggtat tggca 45

<210> 200  
 <211> 2372  
 <212> DNA  
 <213> Homo sapiens

<400> 200  
 agcagggaaa tccggatgtc tcggttatga agtggagcag tgagtgtgag cctcaacata 60  
 gttccagaac tctccatccg gactagttat tgagcatctg cctctcatat caccagtggc 120  
 catctgaggt gtttcccttg ctctgaaggg gtaggcacga tggccagggtg cttcagcctg 180  
 gtgttgcttc tcaacttccat ctggaccacg aggcctcctg tccaaggctc tttgcgtgca 240  
 gaagagcttt ccatccaggt gtcattgcaga attatgggga tcacccttgt gagcaaaaag 300  
 gcgaaccagc agctgaattt cacagaagct aaggaggcct gtaggctgct gggactaagt 360  
 ttggccggca aggaccaagt tgaaacagcc ttgaaagcta gctttgaaac ttgcagctat 420  
 ggctgggttg gagatggatt cgtggtcac tctaggatta gcccaaacc caagtgtggg 480  
 aaaaatgggg tgggtgtcct gatttggaag gttccagtga gccgacagtt tgcagcctat 540  
 tgttacaact catctgatac ttggactaac tcgtgcattc cagaaattat caccaccaa 600  
 gatcccatat tcaacactca aactgcaaca caaacaacag aatttattgt cagtgcagct 660  
 acctactcgg tggcatcccc ttactctaca atacctgcc ctactactac tcctcctgct 720  
 ccagcttcca cttctattcc acggagaaaa aaattgattt gtgtcacaga agtttttatg 780  
 gaaactagca ccatgtctac agaaactgaa ccatttggtg aaaataaagc agcattcaag 840  
 aatgaagctg ctgggttttg aggtgtcccc acggctctgc tagtgcttgc tctcctcttc 900  
 tttggtgctg cagctgggtc tggattttgc tatgtcaaaa ggtatgtgaa ggcttccct 960  
 ttacaaaaca agaatacagca gaaggaaatg atcgaaacca aagtagtaaa ggaggagaag 1020  
 gccaatgata gcaaccctaa tgaggaatca aagaaaactg ataaaaacc agaagagtcc 1080  
 aagagtccaa gcaaaactac cgtgcgatgc ctggaagctg aagtttagat gagacagaaa 1140  
 tgaggagaca cacctgaggc tgggttcttt catgctcctt accctgcccc agctggggaa 1200  
 atcaaaaggg ccaaagaacc aaagaagaaa gtccaccctt ggctcctaac tggaaatcagc 1260  
 tcaggactgc cattggacta tggagtgcac caaagagaat gcccttctcc ttattgtaac 1320  
 cctgtctgga tctatctc ctacctcaa agcttcccac ggcttttcta gctgggtat 1380  
 gtcctaataa tatccactg ggagaaagga gttttgcaaa gtgcaaggac ctaaacatc 1440



```

tcatcagtat ccagtggtaa aaaggcctcc tggctgtctg aggctaggtg gggttgaaagc 1500
caaggagtca ctgagaccaa ggctttctct actgattccg cagctcagac cctttcttca 1560
gctctgaaag agaaacacgt atcccacctg acatgtcctt ctgagcccgg taagagcaaa 1620
agaatggcag aaaagtttag cccctgaaag ccatggagat tctcataact tgagacctaa 1680
tctctgtaaa gctaaaataa agaaatagaa caaggctgag gatacgacag tacactgtca 1740
gcagggactg taaacacaga caggggtcaaa gtgttttctc tgaacacatt gagttggaat 1800
cactgttttag aacacacaca cttacttttt ctggtctcta ccactgctga tattttctct 1860
aggaaatata cttttacaag taacaaaaat aaaaactctt ataaatttct atttttatct 1920
gagttacaga aatgattact aaggaagatt actcagtaat ttgttttaaaa agtaataaaa 1980
ttcaacaaac atttgctgaa tagctactat atgtcaagtg ctgtgcaagg tattacactc 2040
tgtaattgaa tattattcct caaaaaattg cacatagtag aacgctatct gggaagctat 2100
ttttttcagt tttgatattt ctagcttata tacttccaaa ctaattttta tttttgctga 2160
gactaatctt attcattttc tctaatatgg caaccattat aaccttaatt tattattaac 2220
atacctaaga agtacattgt tacctctata taccaaagca catttttaaaa gtgccattaa 2280
caaatgtatc actagccctc ctttttccaa caagaaggga ctgagagatg cagaaatatt 2340
tgtgacaaaa aattaaagca tttagaaaac tt 2372

```

<210> 201

<211> 322

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic protein

<400> 201

```

Met Ala Arg Cys Phe Ser Leu Val Leu Leu Leu Thr Ser Ile Trp Thr
  1                      5                      10                      15

```

```

Thr Arg Leu Leu Val Gln Gly Ser Leu Arg Ala Glu Glu Leu Ser Ile
          20                      25                      30

```

```

Gln Val Ser Cys Arg Ile Met Gly Ile Thr Leu Val Ser Lys Lys Ala
      35                      40                      45

```

```

Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys Glu Ala Cys Arg Leu Leu
      50                      55                      60

```

```

Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala
      65                      70                      75                      80

```

```

Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Asp Gly Phe Val Val
          85                      90                      95

```

```

Ile Ser Arg Ile Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly
      100                      105                      110

```

```

Val Leu Ile Trp Lys Val Pro Val Ser Arg Gln Phe Ala Ala Tyr Cys
      115                      120                      125

```

```

Tyr Asn Ser Ser Asp Thr Trp Thr Asn Ser Cys Ile Pro Glu Ile Ile
      130                      135                      140

```

09909220.071801

Thr Thr Lys Asp Pro Ile Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr  
 145 150 155 160  
 Glu Phe Ile Val Ser Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser  
 165 170 175  
 Thr Ile Pro Ala Pro Thr Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser  
 180 185 190  
 Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu  
 195 200 205  
 Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala  
 210 215 220  
 Ala Phe Lys Asn Glu Ala Ala Gly Phe Gly Gly Val Pro Thr Ala Leu  
 225 230 235 240  
 Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala Ala Gly Leu Gly Phe  
 245 250 255  
 Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro Phe Thr Asn Lys Asn  
 260 265 270  
 Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu Glu Lys Ala  
 275 280 285  
 Asn Asp Ser Asn Pro Asn Glu Glu Ser Lys Lys Thr Asp Lys Asn Pro  
 290 295 300  
 Glu Glu Ser Lys Ser Pro Ser Lys Thr Thr Val Arg Cys Leu Glu Ala  
 305 310 315 320  
 Glu Val

<210> 202

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 202

gagctttcca tccaggtgtc atgc

24

<210> 203

<211> 22

<212> DNA

<213> Artificial Sequence

09909320-071801

<221> modified base

&lt;222&gt; (1003)

&lt;223&gt; a, t, c or g

&lt;400&gt; 206

```

agatggcggg cttggcacct ctaattgctc tcgtgtattc ggtgcgcgga ctttcacgat 60
ggctcgccca accttactac cttctgtcgg ccctgctctc tgctgccttc ctactcgtga 120
ggaaactgcc gccgctctgc cacggctctgc ccacccaacg cgaagacggg aaccgcgttg 180
actttgactg gagagaagtg gagatcctga tgtttctcag tgccattgtg atgatgaaga 240
accgcagatc catcactgtg gagcaacata taggcaacat tttcatgttt agtaaagtgg 300
ccaacacaat tcttttcttc cgcttgataa ttgcgatggg cctactttac atcacactct 360
gcatagtgtt cctgatgacg tgcaaaccac ccctatatat gggccctgag tatatcaagt 420
acttcaatga taaaaccatt gatgaggaac tagaacggga caagaggggc acttggattg 480
tggagtctct tgccaattgg tctaattgact gccaatcatt tgcccctatc tatgctgacc 540
tctcccttaa atacaactgt acagggctaa attttgggaa ggtggatgtt ggacgctata 600
ctgatgttag tacgcgggtac aaagttagca catcacccct caccaagcaa ctccctaccc 660
tgatcctgtt ccaaggtggc aaggaggcaa tgccggcgcc acagattgac aagaaaggac 720
gggctgtctc atggaccttc tctgaggaga atgtgatccg agaatttaac ttaaattgagc 780
tataccagcg ggccaagaaa ctatcaaagg ctggagacaa tatccctgag gagcagcctg 840
tggcttcaac ccccaccaca gtgtcagatg gggaaaacaa gaaggataaa taagatcctc 900
actttggcag tgcttctctc cctgtcaatt ccaggctctt tccataacca caagcctgag 960
gctgcagcct ttnattnatg ttttcccttt ggtgngact ggntggggca gcatgcagct 1020
tctgatttta aagaggcatc tagggaattg tcaggcaccc tacaggaagg cctgccatgc 1080
tgtggccaac tgtttactg gagcaagaaa gagatctcat aggacggagg gggaaatggg 1140
ttccctccaa gcttgggtca gtgtgttaac tgcttatcag ctattcagac atctccatgg 1200
tttctccatg aaactctgtg gtttcatcat tccttcttag ttgacctgca cagcttgggt 1260
agacctagat ttaaccctaa ggtaagatgc tggggtatag aacgctaaga attttcccc 1320
aaggactctt gcttccctaa gcccttctgg ctctgtttat ggtcttcatt aaaagtataa 1380
gcctaacttt gtcgctagtc ctaaggagaa acctttaacc acaaagtttt tatcattgaa 1440
gacaatattg aacaaccccc tattttgtgg ggattgagaa ggggtgaata gaggcttgag 1500
actttccttt gtgtggtagg acttggagga gaaatccctt ggactttcac taacctctg 1560
acatactccc cacaccaggt tgatggcttt ccgtaataaa aagattggga tttcctttt 1620

```

&lt;210&gt; 207

&lt;211&gt; 296

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 207

Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg

1 5 10 15

Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu

20 25 30

Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly

35 40 45

Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg

50 55 60

Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn

65 70 75 80

T08T20" 02E60650

Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe  
                             85                            90                            95  
 Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met  
                             100                            105                            110  
 Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys  
                             115                            120                            125  
 Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Lys Tyr Phe Asn Asp Lys  
                             130                            135                            140  
 Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg Val Thr Trp Ile Val  
 145                            150                            155                            160  
 Glu Phe Phe Ala Asn Trp Ser Asn Asp Cys Gln Ser Phe Ala Pro Ile  
                             165                            170                            175  
 Tyr Ala Asp Leu Ser Leu Lys Tyr Asn Cys Thr Gly Leu Asn Phe Gly  
                             180                            185                            190  
 Lys Val Asp Val Gly Arg Tyr Thr Asp Val Ser Thr Arg Tyr Lys Val  
                             195                            200                            205  
 Ser Thr Ser Pro Leu Thr Lys Gln Leu Pro Thr Leu Ile Leu Phe Gln  
                             210                            215                            220  
 Gly Gly Lys Glu Ala Met Arg Arg Pro Gln Ile Asp Lys Lys Gly Arg  
 225                            230                            235                            240  
 Ala Val Ser Trp Thr Phe Ser Glu Glu Asn Val Ile Arg Glu Phe Asn  
                             245                            250                            255  
 Leu Asn Glu Leu Tyr Gln Arg Ala Lys Lys Leu Ser Lys Ala Gly Asp  
                             260                            265                            270  
 Asn Ile Pro Glu Glu Gln Pro Val Ala Ser Thr Pro Thr Thr Val Ser  
                             275                            280                            285  
 Asp Gly Glu Asn Lys Lys Asp Lys  
                             290                            295

<210> 208

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 208

gcttgatata tcgcatgggc ctac

<210> 209  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 209  
 tggagacaat atccctgagg 20

<210> 210  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 210  
 aacagttggc cacagcatgg cagg 24

<210> 211  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 211  
 ccattgatga ggaactagaa cgggacaaga gggtcacttg gattgtggag 50

<210> 212  
 <211> 1985  
 <212> DNA  
 <213> Homo sapiens

<400> 212  
 ggacagctcg cggcccccca gagctctagc cgtcgaggag ctgcctgggg acgtttgccc 60  
 tggggcccca gcctggcccg ggtcaccctg gcatgaggag atgggcctgt tgctcctggt 120  
 cccattgctc ctgctgcccg gtcctacgg actgcccttc tacaacgggt tctactactc 180  
 caacagcgcc aacgaccaga acctaggcaa cggatcatggc aaagacctcc ttaatggagt 240  
 gaagctgggtg gtggagacac ccgaggagac cctgttcacc taccaagggg ccagtgtgat 300  
 cctgccctgc cgtaccgct acgagccggc cctgggtctcc ccgcggcgtg tgcgtgtcaa 360  
 atggtggaag ctgtcggaga acggggcccc agagaaggac gtgctggtgg ccatcgggct 420  
 gaggcaccgc tcctttgggg actaccaagg ccgcgtgcac ctgcggcagg acaaagagca 480  
 tgacgtctcg ctggagatcc aggatctgcg gctggaggac tatgggcgtt accgctgtga 540  
 ggtcattgac gggctggagg atgaaagcgg tctggtggag ctggagctgc ggggtgtggt 600

FOBT/20-02E60660

ctttcccttac cagtccccca acgggcgcta ccagttcaac ttccacgagg gccagcaggt 660  
 ctgtgcagag caggctgcgg tggtagcctc ctttgagcag ctcttcggg cctgggagga 720  
 gggcctggac tggtagaacg cgggctggct gcaggatgct acgggtgcagt accccatcat 780  
 gttgccccgg cagccctgcg gtggcccagg cctggcacct ggcgtgcgaa gctacggccc 840  
 ccgccaccgc cgcctgcacc gctatgatgt attctgcttc gctactgccc tcaaggggcg 900  
 ggtgtactac ctggagcacc ctgagaagct gacgctgaca gaggcaaggg aggcctgcca 960  
 ggaagatgat gccacgatcg ccaagggtggg acagctcttt gccgcctgga agttccatgg 1020  
 cctggaccgc tgcgacgtg gctggctggc agatggcagc gtccgctacc ctgtggttca 1080  
 cccgcatact aactgtgggc cccagagacc tggggtccga agctttggct tccccgacct 1140  
 gcagagccgc ttgtacgggtg tttactgcta ccgccagcac taggacctgg ggccctcccc 1200  
 tgccgcattc cctcactggc tgtgtattta ttgagtgggt cgttttccct tgtgggttgg 1260  
 agccatttta actgttttta tacttctcaa tttaaatttt ctttaaacad ttttttacta 1320  
 ttttttgtaa agcaaacaga acccaatgcc tccctttgct cctggatgcc ccactccagg 1380  
 aatcatgctt gctccccctgg gccatttgcg gttttgtggg cttctggagg gttccccgcc 1440  
 atccaggctg gtctccctcc cttaaggagg ttggtgcccga gaggggcgcg tggcctgtct 1500  
 agaatgccgc cgggagtcgc ggcattgggtg gcacagttct ccctgcccct cagcctgggg 1560  
 gaagaagagg gcctcggggg cctccggagc tgggcttttg gcctctcctg cccacctcta 1620  
 cttctctgtg aagccgctga cccagtcctg cccactgagg ggctagggtc ggaagccagt 1680  
 tctaggcttc caggcgaaat ctgagggaag gaagaaactc ccctccccgt tccccctccc 1740  
 ctctcggttc caaagaatct gtttgtgtgt catttgtttc tctgtttcc ctgtgtgggg 1800  
 aggggcccctc aggtgtgtgt actttggaca ataaatgggtg ctatgactgc cttccgccaa 1860  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1920  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1980  
 aaaaaa 1985

<210> 213

<211> 360

<212> PRT

<213> Homo sapiens

<400> 213

Met Gly Leu Leu Leu Val Pro Leu Leu Leu Leu Pro Gly Ser Tyr  
 1 5 10 15

Gly Leu Pro Phe Tyr Asn Gly Phe Tyr Tyr Ser Asn Ser Ala Asn Asp  
 20 25 30

Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu Leu Asn Gly Val Lys  
 35 40 45

Leu Val Val Glu Thr Pro Glu Glu Thr Leu Phe Thr Tyr Gln Gly Ala  
 50 55 60

Ser Val Ile Leu Pro Cys Arg Tyr Arg Tyr Glu Pro Ala Leu Val Ser  
 65 70 75 80

Pro Arg Arg Val Arg Val Lys Trp Trp Lys Leu Ser Glu Asn Gly Ala  
 85 90 95

Pro Glu Lys Asp Val Leu Val Ala Ile Gly Leu Arg His Arg Ser Phe  
 100 105 110

Gly Asp Tyr Gln Gly Arg Val His Leu Arg Gln Asp Lys Glu His Asp

1301-02E60660

115					120					125						
Val	Ser	Leu	Glu	Ile	Gln	Asp	Leu	Arg	Leu	Glu	Asp	Tyr	Gly	Arg	Tyr	
130					135					140						
Arg	Cys	Glu	Val	Ile	Asp	Gly	Leu	Glu	Asp	Glu	Ser	Gly	Leu	Val	Glu	
145					150					155					160	
Leu	Glu	Leu	Arg	Gly	Val	Val	Phe	Pro	Tyr	Gln	Ser	Pro	Asn	Gly	Arg	
165					170					175						
Tyr	Gln	Phe	Asn	Phe	His	Glu	Gly	Gln	Gln	Val	Cys	Ala	Glu	Gln	Ala	
180					185					190						
Ala	Val	Val	Ala	Ser	Phe	Glu	Gln	Leu	Phe	Arg	Ala	Trp	Glu	Glu	Gly	
195					200					205						
Leu	Asp	Trp	Cys	Asn	Ala	Gly	Trp	Leu	Gln	Asp	Ala	Thr	Val	Gln	Tyr	
210					215					220						
Pro	Ile	Met	Leu	Pro	Arg	Gln	Pro	Cys	Gly	Gly	Pro	Gly	Leu	Ala	Pro	
225					230					235					240	
Gly	Val	Arg	Ser	Tyr	Gly	Pro	Arg	His	Arg	Arg	Leu	His	Arg	Tyr	Asp	
245					250					255						
Val	Phe	Cys	Phe	Ala	Thr	Ala	Leu	Lys	Gly	Arg	Val	Tyr	Tyr	Leu	Glu	
260					265					270						
His	Pro	Glu	Lys	Leu	Thr	Leu	Thr	Glu	Ala	Arg	Glu	Ala	Cys	Gln	Glu	
275					280					285						
Asp	Asp	Ala	Thr	Ile	Ala	Lys	Val	Gly	Gln	Leu	Phe	Ala	Ala	Trp	Lys	
290					295					300						
Phe	His	Gly	Leu	Asp	Arg	Cys	Asp	Ala	Gly	Trp	Leu	Ala	Asp	Gly	Ser	
305					310					315					320	
Val	Arg	Tyr	Pro	Val	Val	His	Pro	His	Pro	Asn	Cys	Gly	Pro	Pro	Glu	
325					330					335						
Pro	Gly	Val	Arg	Ser	Phe	Gly	Phe	Pro	Asp	Pro	Gln	Ser	Arg	Leu	Tyr	
340					345					350						
Gly	Val	Tyr	Cys	Tyr	Arg	Gln	His									
355					360											

&lt;210&gt; 214

&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

FOOTNOTES



<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 214

tgcttcgcta ctgccctc

18

<210> 215

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 215

ttcccttggtg ggttgag

18

<210> 216

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 216

agggctggaa gccagttc

18

<210> 217

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 217

agccagtgtg gaaatgctg

18

<210> 218

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 218

tgtccaaagt acacacacct gagg

24

1309320-071301

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

45

<400>	220						
ggagagcggga	gcgaagctgg	ataacagggg	accgatgatg	tggcgaccat	cagttctgct	60	
gcttctgttg	ctactgaggc	acggggccca	ggggaagcca	tccccagacg	caggccctca	120	
tggccagggg	aggggtgcacc	aggcggcccc	cctgagcgac	gctccccatg	atgacgcca	180	
cgggaacttc	cagtacgacc	atgaggcttt	cctgggacgg	gaagtggcca	aggaattcga	240	
ccaactcacc	ccagaggaaa	gccaggcccc	tctggggcgg	atcgtggacc	gcatggaccg	300	
cgcggggggac	ggcgacggct	gggtgtcgct	ggccgagctt	cgcgcgtgga	tcgcgcacac	360	
gcagcagcgg	cacatacggg	actcggtgag	cgcggcctgg	gacacgtacg	acacggaccg	420	
cgacgggcgt	gtgggttggg	aggagctgcg	caacgccacc	tatggccact	acgcgcccgg	480	
tgaagaattt	catgacgtgg	aggatgcaga	gacctacaa	aagatgctgg	ctcgggacga	540	
gcggcgtttc	cgggtggccg	accaggatgg	ggactcgatg	gccactcgag	aggagctgac	600	
agccttcctg	caccccgagg	agttccctca	catgcgggac	atcgtgattg	ctgaaacctc	660	
ggaggacctg	gacagaaaaca	aagatggcta	tgtccaggtg	gaggagtaca	tcgcggatct	720	
gtactcagcc	gagcctgggg	aggaggagcc	ggcgtgggtg	cagacggaga	ggcagcagtt	780	
ccgggacttc	cgggatctga	acaaggatgg	gcacctggat	gggagtgagg	tgggccactg	840	
ggtgctgccc	cctgccccagg	accagccccct	ggtggaagcc	aaccacctgc	tgcacgagag	900	
cgacacggac	aaggatgggc	ggctgagcaa	agcggaaatc	ctgggtaatt	ggaacatgtt	960	
tgtgggcagt	caggccacca	actatggcga	ggacctgacc	cggcaccacg	atgagctgtg	1020	
agcaccgcgc	acctgccaca	gcctcagagg	ccgcacaaat	gaccggagga	ggggccgctg	1080	
tggctctggcc	ccctccctgt	ccaggccccc	caggaggcgag	atgcagtcct	aggcatcctc	1140	
ctgcccttg	gctctcagg	acccccctgg	tcggcttctg	tccctgtcac	accccccaacc	1200	
ccaggggagg	gctgtcatag	tcccagagga	taagcaatac	ctattttctga	ctgagtctcc	1260	
cagcccagac	ccagggaccc	ttggccccc	gctcagctct	aagaaccgcc	ccaacccctc	1320	
cagctccaaa	tctgagcctc	caccacatag	actgaaactc	ccctggcccc	agccctctcc	1380	
tgcttggcct	ggcctgggac	acctcctctc	tgccaggagg	caataaaaagc	cagcgccggg	1440	
accttgaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	1500	
aaa						1503	

```
<210> 221
<211> 328
<212> PRT
<213> Homo sapiens
```

<400> 221  
Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Arg His

**SECRET**

1			5						10				15			
Gly	Ala	Gln	Gly	Lys	Pro	Ser	Pro	Asp	Ala	Gly	Pro	His	Gly	Gln	Gly	
		20					25						30			
Arg	Val	His	Gln	Ala	Ala	Pro	Leu	Ser	Asp	Ala	Pro	His	Asp	Asp	Ala	
		35					40						45			
His	Gly	Asn	Phe	Gln	Tyr	Asp	His	Glu	Ala	Phe	Leu	Gly	Arg	Glu	Val	
		50			55						60					
Ala	Lys	Glu	Phe	Asp	Gln	Leu	Thr	Pro	Glu	Glu	Ser	Gln	Ala	Arg	Leu	
		65			70				75						80	
Gly	Arg	Ile	Val	Asp	Arg	Met	Asp	Arg	Ala	Gly	Asp	Gly	Asp	Gly	Trp	
			85						90				95			
Val	Ser	Leu	Ala	Glu	Leu	Arg	Ala	Trp	Ile	Ala	His	Thr	Gln	Gln	Arg	
			100				105						110			
His	Ile	Arg	Asp	Ser	Val	Ser	Ala	Ala	Trp	Asp	Thr	Tyr	Asp	Thr	Asp	
		115					120				125					
Arg	Asp	Gly	Arg	Val	Gly	Trp	Glu	Glu	Leu	Arg	Asn	Ala	Thr	Tyr	Gly	
		130			135						140					
His	Tyr	Ala	Pro	Gly	Glu	Glu	Phe	His	Asp	Val	Glu	Asp	Ala	Glu	Thr	
		145			150				155						160	
Tyr	Lys	Lys	Met	Leu	Ala	Arg	Asp	Glu	Arg	Arg	Phe	Arg	Val	Ala	Asp	
			165						170				175			
Gln	Asp	Gly	Asp	Ser	Met	Ala	Thr	Arg	Glu	Glu	Leu	Thr	Ala	Phe	Leu	
			180				185						190			
His	Pro	Glu	Glu	Phe	Pro	His	Met	Arg	Asp	Ile	Val	Ile	Ala	Glu	Thr	
		195					200				205					
Leu	Glu	Asp	Leu	Asp	Arg	Asn	Lys	Asp	Gly	Tyr	Val	Gln	Val	Glu	Glu	
		210			215						220					
Tyr	Ile	Ala	Asp	Leu	Tyr	Ser	Ala	Glu	Pro	Gly	Glu	Glu	Glu	Pro	Ala	
		225			230				235						240	
Trp	Val	Gln	Thr	Glu	Arg	Gln	Gln	Phe	Arg	Asp	Phe	Arg	Asp	Leu	Asn	
			245						250				255			
Lys	Asp	Gly	His	Leu	Asp	Gly	Ser	Glu	Val	Gly	His	Trp	Val	Leu	Pro	
			260				265						270			
Pro	Ala	Gln	Asp	Gln	Pro	Leu	Val	Glu	Ala	Asn	His	Leu	Leu	His	Glu	
		275					280				285					

Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly  
 290 295 300

Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp  
 305 310 315 320

Leu Thr Arg His His Asp Glu Leu  
 325

<210> 222

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 222

cgcaggccct catggccagg

20

<210> 223

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 223

gaaatcctgg gtaattgg

18

<210> 224

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 224

gtgcgcggtg ctcacagctc atc

23

<210> 225

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

TC8T70" 02E60660

<400> 225  
 cccccctgag cgacgctccc ccatgatgac gcccacggga actt

44

<210> 226  
 <211> 2403  
 <212> DNA  
 <213> Homo sapiens

<400> 226  
 ggggccttgc cttccgcact cgggcgcagc cgggtggatc tcgagcaggt gcgagagcccc 60  
 gggcgggcggg cgcgggtgag agggatccct gacgcctctg tccctgtttc tttgtcgctc 120  
 ccagcctgtc tgtcgctcgtt ttggcgcccc cgcctccccg cgggtgcgggg ttgcacaccg 180  
 atcctgggct tcgctcgatt tgccgcagag gcgcctccca gacctagagg ggcgctggcc 240  
 tggagcagcg ggtcgtctgt gtccctctctc ctctgcgcgc cgcgcgggga tccgaagggt 300  
 gcggggctct gaggaggtga cgcgcggggc ctcccgacc ctggccttgc ccgcattctc 360  
 cctctctccc aggtgtgagc agcctatcag tcacatgtc cgcagcctgg atcccggtc 420  
 tcggcctcgg tgtgtgtctg ctgctgctgc cggggccccg gggcagcgag ggagccgctc 480  
 ccattgctat cacatgtttt accagaggct tggacatcag gaaagagaaa gcagatgtcc 540  
 tctgccaggg gggctgcctt cttgaggaat tctctgtgta tgggaacata gtatatgctt 600  
 ctgtatcgag catatgtggg gctgctgtcc acaggggagt aatcagcaac tcagggggac 660  
 ctgtacgagt ctatagccta cctggtcgag aaaactattc ctcagtagat gccaatggca 720  
 tccagtctca aatgctttct agatggctct cttctttcac agtaactaaa ggcaaaagta 780  
 gtacacagga ggccacagga caagcagtgt ccacagcaca tccaccaaca ggtaaacgac 840  
 taaagaaaac acccgagaag aaaactggca ataaagattg taaagcagac attgcatttc 900  
 tgattgatgg aagctttaat attgggcagc gccgatttaa tttacagaag aattttgttg 960  
 gaaaagtggc tctaattgtt ggaattggaa cagaaggacc acatgtgggc cttgttcaag 1020  
 ccagtgaaca tcccaaaata gaattttact tgaaaaactt tacatcagcc aaagatgttt 1080  
 tgtttgccat aaaggaagta ggtttcagag ggggtaattc caatacagga aaagccttga 1140  
 agcatactgc tcagaaattc ttcacggtag atgctggagt aagaaaaggg atcccaaaag 1200  
 tgggtggtggt atttattgat gggtggcctt ctgatgacat cgaggaagca ggcattgtgg 1260  
 ccagagagtt tgggtgtcaat gtatttatag tttctgtggc caagcctatc cctgaagaac 1320  
 tggggatggt tcaggatgtc acatttgttg acaaggctgt ctgtcggaat aatggcttct 1380  
 tctcttacca catgcccac tggtttggca ccacaaaata cgtaaagcct ctggtacaga 1440  
 agctgtgcac tcatgaacaa atgatgtgca gcaagacctg ttataactca gtgaacattg 1500  
 cctttctaata tgatggctcc agcagtgttg gagatagcaa tttccgcctc atgcttgaat 1560  
 ttgtttccaa catagccaag acttttgaaa tctcggacat tggtgccaag atagctgctg 1620  
 tacagtttac ttatgatcag cgcacggagt tcagtttcac tgactatagc accaaagaga 1680  
 atgtcctagc tgtcatcaga aacatccgct atatgagtgg tggacagct actggtgatg 1740  
 ccatttcctt cactgttaga aatgtgtttg gccctataag ggagagcccc aacaagaact 1800  
 tccatagtaat tgtcacagat gggcagtcct atgatgatgt ccaaggccct gcagctgctg 1860  
 cacatgatgc aggaatcact atcttctctg ttggtgtggc ttgggcacct ctggatgacc 1920  
 tgaaagatat ggcttctaaa ccgaaggagt ctcacgcttt cttcacaaga gagtccacag 1980  
 gattagaacc aattgtttct gatgtcatca gaggcatttg tagagatttc ttagaatccc 2040  
 agcaataatg gtaacathtt gacaactgaa agaaaaagta caaggggatc cagtgtgtaa 2100  
 attgtattct cataatactg aaatgcttta gcatactaga atcagatata aaactattaa 2160  
 gtatgtcaac agccatttag gcaataaagc actcctttta agccgctgcc ttctggttac 2220  
 aatttacagt gtactttgtt aaaaacactg ctgaggtctc ataactatgg ctcttagaaa 2280  
 ctcaggaaag aggagataat gtggattaaa accttaagag ttctaaccat gcctactaaa 2340  
 tgtacagata tgcaaatcc atagctcaat aaaagaatct gatacttaga ccaaaaaaaa 2400  
 aaa 2403

<210> 227

FOR 20" Q2E60660

<213> Homo sapiens

Asn Ser Asn Thr Gly Lys Ala Leu Lys His Thr Ala Gln Lys Phe Phe  
245 250 255

Thr	Val	Asp	Ala	Gly	Val	Arg	Lys	Gly	Ile	Pro	Lys	Val	Val	Val	
			260					265					270		
Phe	Ile	Asp	Gly	Trp	Pro	Ser	Asp	Asp	Ile	Glu	Glu	Ala	Gly	Ile	Val
		275					280					285			
Ala	Arg	Glu	Phe	Gly	Val	Asn	Val	Phe	Ile	Val	Ser	Val	Ala	Lys	Pro
		290				295					300				
Ile	Pro	Glu	Glu	Leu	Gly	Met	Val	Gln	Asp	Val	Thr	Phe	Val	Asp	Lys
305					310					315					320
Ala	Val	Cys	Arg	Asn	Asn	Gly	Phe	Phe	Ser	Tyr	His	Met	Pro	Asn	Trp
				325					330					335	
Phe	Gly	Thr	Thr	Lys	Tyr	Val	Lys	Pro	Leu	Val	Gln	Lys	Leu	Cys	Thr
			340					345					350		
His	Glu	Gln	Met	Met	Cys	Ser	Lys	Thr	Cys	Tyr	Asn	Ser	Val	Asn	Ile
		355					360					365			
Ala	Phe	Leu	Ile	Asp	Gly	Ser	Ser	Ser	Val	Gly	Asp	Ser	Asn	Phe	Arg
		370				375					380				
Leu	Met	Leu	Glu	Phe	Val	Ser	Asn	Ile	Ala	Lys	Thr	Phe	Glu	Ile	Ser
385					390					395					400
Asp	Ile	Gly	Ala	Lys	Ile	Ala	Ala	Val	Gln	Phe	Thr	Tyr	Asp	Gln	Arg
				405					410					415	
Thr	Glu	Phe	Ser	Phe	Thr	Asp	Tyr	Ser	Thr	Lys	Glu	Asn	Val	Leu	Ala
			420					425					430		
Val	Ile	Arg	Asn	Ile	Arg	Tyr	Met	Ser	Gly	Gly	Thr	Ala	Thr	Gly	Asp
		435					440					445			
Ala	Ile	Ser	Phe	Thr	Val	Arg	Asn	Val	Phe	Gly	Pro	Ile	Arg	Glu	Ser
		450				455					460				
Pro	Asn	Lys	Asn	Phe	Leu	Val	Ile	Val	Thr	Asp	Gly	Gln	Ser	Tyr	Asp
465					470					475					480
Asp	Val	Gln	Gly	Pro	Ala	Ala	Ala	Ala	His	Asp	Ala	Gly	Ile	Thr	Ile
				485					490					495	
Phe	Ser	Val	Gly	Val	Ala	Trp	Ala	Pro	Leu	Asp	Asp	Leu	Lys	Asp	Met
			500					505					510		
Ala	Ser	Lys	Pro	Lys	Glu	Ser	His	Ala	Phe	Phe	Thr	Arg	Glu	Phe	Thr
		515					520					525			
Gly	Leu	Glu	Pro	Ile	Val	Ser	Asp	Val	Ile	Arg	Gly	Ile	Cys	Arg	Asp
	530					535					540				

Phe Leu Glu Ser Gln Gln  
545 550

<210> 228

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 228

tggtctcgca caccgatc

18

<210> 229

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 229

ctgctgtcca caggggag

18

<210> 230

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 230

ccttgaagca tactgctc

18

<210> 231

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 231

gagatagcaa tttccgcc

18

<210> 232

09909320.071801



<211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 232  
 ttctctcaaga gggcagcc

18

<210> 233  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 233  
 cttggcacca atgtccgaga tttc

24

<210> 234  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 234  
 gctctgagga aggtgacgcg cggggcctcc gaacccttgg ccttg

45

<210> 235  
 <211> 2586  
 <212> DNA  
 <213> Homo sapiens

<400> 235  
 cgccgcgctc ccgcacccgc ggccccccca ccgcgcccgt cccgcacctg caccgcagc 60  
 ccggcggcct ccggcgggga gcgagcagat ccagtccggc ccgcagcgca actcggtcca 120  
 gtcggggcgg cggctgcggg cgcagagcgg agatgcagcg gcttggggcc accctgctgt 180  
 gcctgctgct ggcggcgggc gtccccacgg cccccgcgcc cgctccgacg gcgacctcgg 240  
 ctccagtcaa gcccggcccc gctctcagct acccgcagga ggaggccacc ctcaatgaga 300  
 tgttccgcga gggtgaggaa ctgatggagg acacgcagca caaattgcgc agcgcggtgg 360  
 aagagatgga ggcagaagaa gctgctgcta aagcatcatc agaagtgaac ctggcaaact 420  
 tacctcccag ctatcacaat gagaccaaca cagacacgaa gggttggaat aataccatcc 480  
 atgtgcaccg agaaattcac aagataacca acaaccagac tggacaaatg gtcttttcag 540  
 agacagttat cacatctgtg ggagacgaag aaggcagaag gagccacgag tgcacatcgc 600  
 acgaggactg tgggcccagc atgtactgcc agtttgccag cttccagtac acctgccagc 660  
 catgccgggg ccagaggatg ctctgcaccc gggacagtga gtgctgtgga gaccagctgt 720

099093002260660

gtgtctgggg tcaactgcacc aaaatggcca ccaggggag caatgggacc atctgtgaca 780  
 accagagga ctgccagccg gggctgtgct gtgccttcca gagaggcctg ctgttccctg 840  
 tgtgcacacc cctgcccgtg gagggcgagc tttgccatga ccccgccagc cggcttcttg 900  
 acctcatcac ctgggagcta gagcctgatg gagccttgga ccgatgccct tgtgccagt 960  
 gcctcctctg ccagccccc agccacagcc tgggtgatgt gtgcaagccg accttcgtgg 1020  
 ggagccgtga ccaagatggg gagatcctgc tgcccagaga ggtccccgat gagtatgaag 1080  
 ttggcagctt catggaggag gtgcgccagg agctggagga cctggagagg agcctgactg 1140  
 aagagatggc gctgggggag cctgcggctg ccgcgcctgc actgctggga ggggaagaga 1200  
 tttagatctg gaccaggctg tgggtagatg tgcaatagaa atagctaatt ttttcccca 1260  
 ggtgtgtgct ttaggcgtgg gctgaccagg cttcttctta catcttcttc ccagtaagtt 1320  
 tccccctctg cttgacagca tgaggtgttg tgcatttggt cagctcccc aggctgttct 1380  
 ccaggcttca cagtctggtg cttgggagag tcaggcaggg ttaaaactgca ggagcagttt 1440  
 gccacccctg tccagattat tggctgcttt gcctctacca gttggcagac agccgtttgt 1500  
 tctacatggc tttgataatt gtttgagggg aggagatgga aacaatgtgg agtctccctc 1560  
 tgattggttt tggggaaatg tggagaagag tgccctgctt tgcaaacatc aacctggcaa 1620  
 aaatgcaaca aatgaatttt ccacgcagtt ctttccatgg gcataggtaa gctgtgcctt 1680  
 cagctgttgc agatgaaatg ttctgttcac cctgcattac atgtgtttat tcatccagca 1740  
 gtgttgctca gctcctacct ctgtgccagg gcagcatttt catatccaag atcaattccc 1800  
 tctctcagca cagcctgggg aggggggtcat tgttctcttc gtccatcagg gatctcagag 1860  
 gctcagagac tgcaagctgc ttgcccaggt cacacagcta gtgaagacca gagcagtttc 1920  
 atctggttgt gactctaagc tcagtgtctc ctccactacc ccacaccagc cttggtgcca 1980  
 ccaaaagtgc tccccaaaag gaaggagaat gggatttttc ttgaggcatg cacatctgga 2040  
 attaaggtca aactaattct cacatccctc taaaagtaaa ctactgttag gaacagcagt 2100  
 gttctcacag tgtggggcag ccgtccttct aatgaagaca atgatattga cactgtccct 2160  
 ctttggcagt tgcattagta actttgaaag gtatatgact gagcgtagca tacagggttaa 2220  
 cctgcagaaa cagtacttag gtaattgtag ggcgaggatt ataaatgaaa tttgcaaaat 2280  
 cacttagcag caactgaaga caattatcaa ccacgtggag aaaatcaaac cgagcagggc 2340  
 tgtgtgaaac atggttgtaa tatgcgactg cgaacactga actctacgcc actccacaaa 2400  
 tgatgttttc aggtgtcatg gactgttgcc accatgtatt catccagagt tcttaaagtt 2460  
 taaagttgca catgattgta taagcatgct ttctttgagt tttaaattat gtataaacat 2520  
 aagttgcatt tagaaatcaa gcataaatca cttcaactgc aaaaaaaaaa aaaaaaaaaa 2580  
 aaaaaa 2586

<210> 236

<211> 350

<212> PRT

<213> Homo sapiens

<400> 236

Met Gln Arg Leu Gly Ala Thr Leu Leu Cys Leu Leu Leu Ala Ala Ala  
 1 5 10 15

Val Pro Thr Ala Pro Ala Pro Ala Pro Thr Ala Thr Ser Ala Pro Val  
 20 25 30

Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn  
 35 40 45

Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys  
 50 55 60

Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys  
 65 70 75 80

Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn  
85 90 95

Glu Thr Asn Thr Asp Thr Lys Val Gly Asn Asn Thr Ile His Val His  
100 105 110

Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe  
115 120 125

Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser  
130 135 140

His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln  
145 150 155 160

Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met  
165 170 175

Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp  
180 185 190

Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys  
195 200 205

Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg  
210 215 220

Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu  
225 230 235 240

Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu  
245 250 255

Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu  
260 265 270

Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe  
275 280 285

Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val  
290 295 300

Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu  
305 310 315 320

Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Gly Glu  
325 330 335

Pro Ala Ala Ala Ala Ala Ala Leu Leu Gly Gly Glu Glu Ile  
340 345 350

&lt;210&gt; 237

FOOT-0-02E60660

<211> 17  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 237  
 ggagctgcac cccttgc

17

<210> 238  
 <211> 49  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 238  
 ggaggactgt gccaccatga gagactcttc aaaccaagg caaaattgg

49

<210> 239  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 239  
 gcagagcggg gatgcagcgg cttg

24

<210> 240  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 240  
 ttggcagctt catggagg

18

<210> 241  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 241  
 cctgggcaaa aatgcaac

18

TOBT 40-0260660

<210> 242  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 242  
 ctccagctcc tggcgcacct cctc

24

<210> 243  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 243  
 ggctctcagc taccgcgag gagcgaggcc accctcaatg agatg

45

<210> 244  
 <211> 3679  
 <212> DNA  
 <213> Homo Sapien

<400> 244  
 aaggaggctg ggaggaaaga ggtaagaaag gttagagaac ctacctcaca 50  
 tctctctggg ctccagaagga ctctgaagat aacaataatt tcagcccatc 100  
 cactctcctt ccttcccaaa cacacatgtg catgtacaca cacacataca 150  
 cacacataca ccttctctct cttcactgaa gactcacagt cactcactct 200  
 gtgagcaggt catagaaaag gacactaaag ccttaaggac aggctggcc 250  
 attacctctg cagctccttt ggcttggtga gtcaaaaaac atgggagggg 300  
 ccaggcacgg tgactcacac ctgtaatccc agcatttttg gagaccgagg 350  
 tgagcagatc acttgagggtc aggagttcga gaccagcctg gccaacatgg 400  
 agaaaccccc atctctacta aaaatacaaa aattagccag gagtgggtggc 450  
 aggtgcctgt aatcccagct actcaggtgg ctgagccagg agaatcgctt 500  
 gaatccagga ggcggaggat gcagtcagct gagtgcaccg ctgcactcca 550  
 gcctgggtga cagaatgaga ctctgtctca aacaaacaaa cacgggagga 600

0509320-071801

ggggtagata ctgcttctct gcaacctcct taactctgca tctctcttctt 650  
 ccagggctgc ccctgatggg gcctggcaat gactgagcag gcccagcccc 700  
 agaggacaag gaagagaagg catattgagg agggcaagaa gtgacgccccg 750  
 gtgtagaatg actgccctgg gaggggtggtt ccttgggccc tggcaggggtt 800  
 gctgaccttt accctgcaaa acacaaagag caggactcca gactctcctt 850  
 gtgaatggtc ccctgccctg cagctccacc atgaggcttc tegtggcccc 900  
 actcttgcta gcttgggtgg ctggtgccac tgccactgtg cccgtggtac 950  
 cctggcätgt tccctgcccc cctcagtgtg cctgccagat ccggccctgg 1000  
 tatacgcccc gctcgtccta ccgcgaggct accactgtgg actgcaatga 1050  
 cctattcctg acggcagtc ccccggcact ccccgcaggc acacagacct 1100  
 tgctcctgca gagcaacagc attgtccgtg tggaccagag tgagctgggc 1150  
 tacctggcca atctcacaga gctggacctg tcccagaaca gcttttcgga 1200  
 tgcccgagac tgtgatttcc atgccctgcc ccagctgctg agcctgcacc 1250  
 tagaggagaa ccagctgacc cggctggagg accacagctt tgcagggctg 1300  
 gccagcctac aggaactcta tctcaaccac aaccagctct accgcatcgc 1350  
 ccccagggcc ttttctggcc tcagcaactt gctgcggctg cacctcaact 1400  
 ccaacctcct gagggccatt gacagccgct ggtttgaaat gctgccaac 1450  
 ttggagatac tcatgattgg cggcaacaag gtagatgcca tcttgacat 1500  
 gaacttccgg cccctggcca acctgcgtag cctggtgcta gcaggcatga 1550  
 acctgcggga gatctccgac tatgccctgg aggggctgca aagcctggag 1600  
 agcctctcct tctatgacaa ccagctggcc cgggtgcca ggcgggcact 1650  
 ggaacagggtg cccgggctca agttcctaga cctcaacaag aaccgctcc 1700  
 agcgggtagg gccgggggac tttgccaaca tgctgcacct taaggagctg 1750  
 ggactgaaca acatggagga gctggtctcc atcgacaagt ttgccctggt 1800  
 gaacctcccc gagctgacca agctggacat caccaataac ccacggctgt 1850  
 ccttcatcca cccccgcgc ttccaccacc tgcccagat ggagaccctc 1900  
 atgctcaaca acaacgctct cagtgccttg caccagcaga cgggtggagtc 1950

cctgccaac ctgcaggagg taggtctcca cggcaacccc atccgctgtg 2000  
 actgtgtcat ccgctggggc aatgccacgg gcacccgtgt ccgcttcac 2050  
 gagccgcaat ccaccctgtg tgcggagcct ccggacctcc agcgccctcc 2100  
 ggtccgtgag gtgcccttcc gggagatgac ggaccactgt ttgcccctca 2150  
 tctccccacg aagcttcccc ccaagcctcc aggtagccag tggagagagc 2200  
 atggtgctgc attgccgggc actggccgaa cccgaacccg agatctactg 2250  
 ggtcactcca gctgggcttc gactgacacc tgcccatgca ggcaggaggt 2300  
 accgggtgta ccccgagggg acctggagc tgcggagggg gacagcagaa 2350  
 gaggcagggc tatacacctg tgtggcccag aacctggtgg gggctgacac 2400  
 taagacggtt agtgtggttg tgggccgtgc tctcctccag ccaggcaggg 2450  
 acgaaggaca ggggctggag ctccgggtgc aggagacca cccctatcac 2500  
 atcctgctat cttgggtcac cccaccaac acagtgtcca ccaacctcac 2550  
 ctggtccagt gcctcctccc tccggggcca gggggccaca gctctggccc 2600  
 gcctgcctcg gggaaccac agctacaaca ttaccgcct ccttcaggcc 2650  
 acggagtact gggcctgcct gcaagtggcc tttgctgatg cccacacca 2700  
 gttggcttgt gtatgggcca ggaccaaaga ggccattct tgccacagag 2750  
 ccttagggga tcgtcctggg ctcatgcca tctggctct cgctgtcctt 2800  
 ctctggcag ctgggctagc ggcccacctt ggcacaggcc aaccaggaa 2850  
 ggggtgtggg gggaggcggc ctctccctcc agcctgggct ttctggggct 2900  
 ggagtgcccc ttctgtccgg gttgtgtctg ctcccctcgt cctgccctgg 2950  
 aatccaggga ggaagctgcc cagatcctca gaaggggaga cactgttgcc 3000  
 accattgtct caaaattctt gaagctcagc ctgttctcag cagtagagaa 3050  
 atcactagga ctacttttta ccaaagaga agcagtctgg gccagatgcc 3100  
 ctgccaggaa agggacatgg acccacgtgc ttgaggcctg gcagctgggc 3150  
 caagacagat ggggctttgt ggccctgggg gtgcttctgc agccttgaaa 3200  
 aagttgccct tacctcctag ggtcacctct gctgccatc tgaggaacat 3250

ctccaaggaa caggaggagac tttggctaga gcctcctgcc tccccatctt 3300  
ctctctgccc agaggctcct gggcctggct tggctgtccc ctacctgtgt 3350  
ccccgggctg cacccttcc tcttctcttt ctctgtacag tctcagttgc 3400  
ttgctcttgt gcctcctggg caagggtga aggaggccac tccatctcac 3450  
ctcggggggc tgccctcaat gtgggagtga cccagccag atctgaagga 3500  
catttgggag agggatgccc aggaacgcct catctcagca gcctgggctc 3550  
ggcattccga agctgacttt ctataggcaa tttgtacct ttgtggagaa 3600  
atgtgtcacc tcccccaacc cgattcactc ttttctcctg ttttgtaaaa 3650  
aataaaaata aataataaca ataaaaaaa 3679

<210> 245

<211> 713

<212> PRT

<213> Homo Sapien

<400> 245

Met	Arg	Leu	Leu	Val	Ala	Pro	Leu	Leu	Leu	Ala	Trp	Val	Ala	Gly	1	5	10	15
Ala	Thr	Ala	Thr	Val	Pro	Val	Val	Pro	Trp	His	Val	Pro	Cys	Pro	20	25	30	
Pro	Gln	Cys	Ala	Cys	Gln	Ile	Arg	Pro	Trp	Tyr	Thr	Pro	Arg	Ser	35	40	45	
Ser	Tyr	Arg	Glu	Ala	Thr	Thr	Val	Asp	Cys	Asn	Asp	Leu	Phe	Leu	50	55	60	
Thr	Ala	Val	Pro	Pro	Ala	Leu	Pro	Ala	Gly	Thr	Gln	Thr	Leu	Leu	65	70	75	
Leu	Gln	Ser	Asn	Ser	Ile	Val	Arg	Val	Asp	Gln	Ser	Glu	Leu	Gly	80	85	90	
Tyr	Leu	Ala	Asn	Leu	Thr	Glu	Leu	Asp	Leu	Ser	Gln	Asn	Ser	Phe	95	100	105	
Ser	Asp	Ala	Arg	Asp	Cys	Asp	Phe	His	Ala	Leu	Pro	Gln	Leu	Leu	110	115	120	
Ser	Leu	His	Leu	Glu	Glu	Asn	Gln	Leu	Thr	Arg	Leu	Glu	Asp	His	125	130	135	
Ser	Phe	Ala	Gly	Leu	Ala	Ser	Leu	Gln	Glu	Leu	Tyr	Leu	Asn	His	140	145	150	

F08F20-02E60660



Asn	Gln	Leu	Tyr	Arg	Ile	Ala	Pro	Arg	Ala	Phe	Ser	Gly	Leu	Ser	
				155					160					165	
Asn	Leu	Leu	Arg	Leu	His	Leu	Asn	Ser	Asn	Leu	Leu	Arg	Ala	Ile	
				170					175					180	
Asp	Ser	Arg	Trp	Phe	Glu	Met	Leu	Pro	Asn	Leu	Glu	Ile	Leu	Met	
				185					190					195	
Ile	Gly	Gly	Asn	Lys	Val	Asp	Ala	Ile	Leu	Asp	Met	Asn	Phe	Arg	
				200					205					210	
Pro	Leu	Ala	Asn	Leu	Arg	Ser	Leu	Val	Leu	Ala	Gly	Met	Asn	Leu	
				215					220					225	
Arg	Glu	Ile	Ser	Asp	Tyr	Ala	Leu	Glu	Gly	Leu	Gln	Ser	Leu	Glu	
				230					235					240	
Ser	Leu	Ser	Phe	Tyr	Asp	Asn	Gln	Leu	Ala	Arg	Val	Pro	Arg	Arg	
				245					250					255	
Ala	Leu	Glu	Gln	Val	Pro	Gly	Leu	Lys	Phe	Leu	Asp	Leu	Asn	Lys	
				260					265					270	
Asn	Pro	Leu	Gln	Arg	Val	Gly	Pro	Gly	Asp	Phe	Ala	Asn	Met	Leu	
				275					280					285	
His	Leu	Lys	Glu	Leu	Gly	Leu	Asn	Asn	Met	Glu	Glu	Leu	Val	Ser	
				290					295					300	
Ile	Asp	Lys	Phe	Ala	Leu	Val	Asn	Leu	Pro	Glu	Leu	Thr	Lys	Leu	
				305					310					315	
Asp	Ile	Thr	Asn	Asn	Pro	Arg	Leu	Ser	Phe	Ile	His	Pro	Arg	Ala	
				320					325					330	
Phe	His	His	Leu	Pro	Gln	Met	Glu	Thr	Leu	Met	Leu	Asn	Asn	Asn	
				335					340					345	
Ala	Leu	Ser	Ala	Leu	His	Gln	Gln	Thr	Val	Glu	Ser	Leu	Pro	Asn	
				350					355					360	
Leu	Gln	Glu	Val	Gly	Leu	His	Gly	Asn	Pro	Ile	Arg	Cys	Asp	Cys	
				365					370					375	
Val	Ile	Arg	Trp	Ala	Asn	Ala	Thr	Gly	Thr	Arg	Val	Arg	Phe	Ile	
				380					385					390	
Glu	Pro	Gln	Ser	Thr	Leu	Cys	Ala	Glu	Pro	Pro	Asp	Leu	Gln	Arg	
				395					400					405	
Leu	Pro	Val	Arg	Glu	Val	Pro	Phe	Arg	Glu	Met	Thr	Asp	His	Cys	

FOBT 20-02E6060

	410		415		420
Leu Pro Leu Ile	Ser Pro Arg Ser Phe	Pro Pro Ser Leu Gln Val			
	425		430		435
Ala Ser Gly Glu	Ser Met Val Leu His	Cys Arg Ala Leu Ala Glu			
	440		445		450
Pro Glu Pro Glu	Ile Tyr Trp Val Thr	Pro Ala Gly Leu Arg Leu			
	455		460		465
Thr Pro Ala His	Ala Gly Arg Arg Tyr	Arg Val Tyr Pro Glu Gly			
	470		475		480
Thr Leu Glu Leu	Arg Arg Val Thr Ala	Glu Glu Ala Gly Leu Tyr			
	485		490		495
Thr Cys Val Ala	Gln Asn Leu Val Gly	Ala Asp Thr Lys Thr Val			
	500		505		510
Ser Val Val Val	Gly Arg Ala Leu Leu	Gln Pro Gly Arg Asp Glu			
	515		520		525
Gly Gln Gly Leu	Glu Leu Arg Val Gln	Glu Thr His Pro Tyr His			
	530		535		540
Ile Leu Leu Ser	Trp Val Thr Pro Pro	Asn Thr Val Ser Thr Asn			
	545		550		555
Leu Thr Trp Ser	Ser Ala Ser Ser Leu	Arg Gly Gln Gly Ala Thr			
	560		565		570
Ala Leu Ala Arg	Leu Pro Arg Gly Thr	His Ser Tyr Asn Ile Thr			
	575		580		585
Arg Leu Leu Gln	Ala Thr Glu Tyr Trp	Ala Cys Leu Gln Val Ala			
	590		595		600
Phe Ala Asp Ala	His Thr Gln Leu Ala	Cys Val Trp Ala Arg Thr			
	605		610		615
Lys Glu Ala Thr	Ser Cys His Arg Ala	Leu Gly Asp Arg Pro Gly			
	620		625		630
Leu Ile Ala Ile	Leu Ala Leu Ala Val	Leu Leu Leu Ala Ala Gly			
	635		640		645
Leu Ala Ala His	Leu Gly Thr Gly Gln	Pro Arg Lys Gly Val Gly			
	650		655		660
Gly Arg Arg Pro	Leu Pro Pro Ala Trp	Ala Phe Trp Gly Trp Ser			
	665		670		675

FOBT 20-0360660

Ala Pro Ser Val Arg Val Val Ser Ala Pro Leu Val Leu Pro Trp  
                                 680                                685                                690

Asn Pro Gly Arg Lys Leu Pro Arg Ser Ser Glu Gly Glu Thr Leu  
                                 695                                700                                705

Leu Pro Pro Leu Ser Gln Asn Ser  
                                 710

<210> 246

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 246

aacaaggtaa gatgccatcc tg 22

<210> 247

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 247

aaacttgctg atggagacca gctc 24

<210> 248

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 248

aggggctgca aagcctggag agcctctcct tctatgacaa ccagc 45

<210> 249

<211> 3401

<212> DNA

<213> Homo Sapien

<400> 249

gcaagccaag gcgctgtttg agaaggtgaa gaagttccgg acccatgtgg 50

aggaggggga catttgtgtac cgcctctaca tgcggcagac catcatcaag 100

gtgatcaagt tcatcctcat catctgtctac accgtctact acgtgcacaa 150

TOBT 20 02E50550

catcaagttc gacgtggact gcaccgtgga cattgagagc ctgacgggct 200  
accgcaccta ccgctgtgcc caccctctgg ccacactctt caagatcctg 250  
gcgtccttct acatcagcct agtcactctt tacggcctca tctgcatgta 300  
cacactgtgg tggatgctac ggcgtccct caagaagtac tcgtttgagt 350  
cgatccgtga ggagagcagc tacagcgaca tccccgacgt caagaacgac 400  
ttcgcttca tgetgcacct cattgaccaa tacgaccgc tctactcaa 450  
gcgttcgcc gtcttctgt cggaggtgag tgagaacaag ctgcggcagc 500  
tgaacctcaa caacgagtgg acgtggaca agctccgga gcggctcacc 550  
aagaacgcgc aggacaagct ggagctgcac ctgttcatgc tcagtggcat 600  
ccctgacact gtgtttgacc tgggtggagct ggaggtctc aagctggagc 650  
tgatccccga cgtgaccatc ccgccagca ttgccagct cacgggcctc 700  
aaggagctgt ggctctacca cacagcggcc aagattgaag cgctgcgt 750  
ggccttctc cgcgagaacc tgcgggcgt gcacatcaag ttcaccgaca 800  
tcaaggagat cccgtgtgg atctatagc tgaagacact ggaggagctg 850  
cacctgacgg gcaacctgag cgcggagaac aaccgtaca tcgtcatcga 900  
cgggctgcgg gagtcaaac gcctcaagg gtgcggctc aagagcaacc 950  
taagcaagct gccacaggtg gtcacagatg tgggcgtgca cctgcagaag 1000  
ctgtccatca acaatgaggg caccaagctc atcgtcctca acagcctcaa 1050  
gaagatggcg aacctgactg agctggagct gatccgtgc gacctggagc 1100  
gcatcccca ctccatctt agctccaca acctgcagga gattgacctc 1150  
aaggacaaca acctcaagac catcgaggag atcatcagct tccagcacct 1200  
gcaccgcctc acctgcctta agctgtggt caaccacatc gcctacatcc 1250  
ccatccagat cggcaacctc accaacctgg agcgcctcta cctgaaccgc 1300  
aacaagatcg agaagatccc caccagctc ttctactgcc gcaagctgcg 1350  
ctacctggac ctacgccaca acaacctgac ctctctcct gccgacatcg 1400  
gcctcctgca gaacctccag aacctagcca tcacggccaa ccggtcag 1450

0909320.071804  
100720026660

acgtccctc cggagctctt ccagtgccgg aagctgcggg cctgcacct 1500  
 gggcaacaac gtgctgcagt cactgccctc caggggtgggc gagctgacca 1550  
 acctgacgca gatcgagctg cggggcaacc ggctggagtg cctgcctgtg 1600  
 gagctgggcg agtgcccact gctcaagcgc agcggcttgg tggaggagga 1650  
 ggacctgttc aacacactgc caccgaggt gaaggagcgg ctgtggaggg 1700  
 ctgacaagga gcaggcctga gcgaggccgg cccagcacag caagcagcag 1750  
 gaccgctgcc cagtccctcag gcccgagggg gcaggcctag cttctcccag 1800  
 aactcccga cagccaggac agcctcgcgg ctgggcagga gcctggggcc 1850  
 gcttgtgagt caggccagag cgagaggaca gtatctgtgg ggctggcccc 1900  
 tttctccct ctgagactca cgtccccag ggcaagtgt tgtggaggag 1950  
 agcaagtctc aagagcgcag tatttgata atcagggtct cctccctgga 2000  
 ggccagctct gcccagggg ctgagctgcc accagaggtc ctgggacct 2050  
 cactttagtt cttggtattt atttttctcc atctcccacc tccttcatcc 2100  
 agataactta tacattccca agaaagttca gccagatgg aaggtgttca 2150  
 gggaaaggtg ggctgccttt tccccttgtc cttatttagc gatgccgcg 2200  
 ggcatttaac acccacctgg acttcagcag agtgggtccg ggccaaccag 2250  
 ccatgggacg gtcaccacgc agtgccgggc tgggctctgc ggtgcggtcc 2300  
 acgggagagc aggcctccag ctggaaaggc caggcctgga gcttgccctc 2350  
 tcagtttttg tggcagtttt agttttttgt ttttttttt tttaatcaaa 2400  
 aaacaatttt ttttaaaaaa aagctttgaa aatggatggg ttgggtatta 2450  
 aaaagaaaaa aaaaacttaa aaaaaaaaag aactaacgg ccagtgagtt 2500  
 ggagtctcag ggcagggtgg cagtttccct tgagcaaagc agccagacgt 2550  
 tgaactgtgt ttcctttccc tgggcgcagg gtgcagggtg tcttccggat 2600  
 ctggtgtgac cttgggtccag gagttctatt tgttccctgg gagggaggtt 2650  
 tttttgtttg ttttttgggt ttttttgggt tcttgttttc tttctcctcc 2700  
 atgtgtcttg gcaggcactc atttctgtgg ctgtcggcca gagggaatgt 2750  
 tctggagctg ccaaggaggg aggagactcg ggttggctaa tccccggatg 2800

aacggtgctc cattcgcacc tcccctcctc gtgcctgccc tgccctctcca 2850  
 cgcacagtgt taaggagcca agaggagcca cttcgcccag actttgtttc 2900  
 cccacctcct gcggcatggg tgtgtccagt gccaccgctg gcctccgctg 2950  
 cttccatcag cctgtgcgc acctggctct tcatgaagag cagacactta 3000  
 gaggtctggtc ggggaatgggg aggtcgcccc tgggagggca ggcgttggtt 3050  
 ccaagccggt tcccgtcctt ggcgcctgga gtgcacacag cccagtcggc 3100  
 acctggtggc tggaagccaa cctgcttttag atcactcggg tccccacctt 3150  
 agaagggctc ccgccttaga tcaatcacgt ggacactaag gcacgtttta 3200  
 gagtctcttg tcttaatgat tatgtccatc cgtctgtccg tccatttggtg 3250  
 tttctcgcgt cgtgtcattg gatataatcc tcagaaataa tgcacactag 3300  
 cctctgacaa ccatgaagca aaaatccggt acatgtgggt ctgaacttgt 3350  
 agactcggtc acagtatcaa ataaaatcta taacagaaaa aaaaaaaaaa 3400  
 a 3401

<210> 250

<211> 546

<212> PRT

<213> Homo Sapien

<400> 250

Met	Arg	Gln	Thr	Ile	Ile	Lys	Val	Ile	Lys	Phe	Ile	Leu	Ile	Ile
1				5					10					15

Cys	Tyr	Thr	Val	Tyr	Tyr	Val	His	Asn	Ile	Lys	Phe	Asp	Val	Asp
				20					25					30

Cys	Thr	Val	Asp	Ile	Glu	Ser	Leu	Thr	Gly	Tyr	Arg	Thr	Tyr	Arg
				35					40					45

Cys	Ala	His	Pro	Leu	Ala	Thr	Leu	Phe	Lys	Ile	Leu	Ala	Ser	Phe
				50					55					60

Tyr	Ile	Ser	Leu	Val	Ile	Phe	Tyr	Gly	Leu	Ile	Cys	Met	Tyr	Thr
				65					70					75

Leu	Trp	Trp	Met	Leu	Arg	Arg	Ser	Leu	Lys	Lys	Tyr	Ser	Phe	Glu
				80					85					90

Ser	Ile	Arg	Glu	Glu	Ser	Ser	Tyr	Ser	Asp	Ile	Pro	Asp	Val	Lys
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

09909320.071301

	95		100		105
Asn Asp Phe Ala	Phe Met Leu His Leu	Ile Asp Gln Tyr Asp	Pro		
	110		115		120
Leu Tyr Ser Lys	Arg Phe Ala Val Phe	Leu Ser Glu Val Ser	Glu		
	125		130		135
Asn Lys Leu Arg	Gln Leu Asn Leu Asn	Asn Glu Trp Thr Leu	Asp		
	140		145		150
Lys Leu Arg Gln	Arg Leu Thr Lys Asn	Ala Gln Asp Lys Leu	Glu		
	155		160		165
Leu His Leu Phe	Met Leu Ser Gly Ile	Pro Asp Thr Val Phe	Asp		
	170		175		180
Leu Val Glu Leu	Glu Val Leu Lys Leu	Glu Leu Ile Pro Asp	Val		
	185		190		195
Thr Ile Pro Pro	Ser Ile Ala Gln Leu	Thr Gly Leu Lys Glu	Leu		
	200		205		210
Trp Leu Tyr His	Thr Ala Ala Lys Ile	Glu Ala Pro Ala Leu	Ala		
	215		220		225
Phe Leu Arg Glu	Asn Leu Arg Ala Leu	His Ile Lys Phe Thr	Asp		
	230		235		240
Ile Lys Glu Ile	Pro Leu Trp Ile Tyr	Ser Leu Lys Thr Leu	Glu		
	245		250		255
Glu Leu His Leu	Thr Gly Asn Leu Ser	Ala Glu Asn Asn Arg	Tyr		
	260		265		270
Ile Val Ile Asp	Gly Leu Arg Glu Leu	Lys Arg Leu Lys Val	Leu		
	275		280		285
Arg Leu Lys Ser	Asn Leu Ser Lys Leu	Pro Gln Val Val Thr	Asp		
	290		295		300
Val Gly Val His	Leu Gln Lys Leu Ser	Ile Asn Asn Glu Gly	Thr		
	305		310		315
Lys Leu Ile Val	Leu Asn Ser Leu Lys	Lys Met Ala Asn Leu	Thr		
	320		325		330
Glu Leu Glu Leu	Ile Arg Cys Asp Leu	Glu Arg Ile Pro His	Ser		
	335		340		345
Ile Phe Ser Leu	His Asn Leu Gln Glu	Ile Asp Leu Lys Asp	Asn		
	350		355		360

T08T20-02E60660

Asn	Leu	Lys	Thr	Ile	Glu	Glu	Ile	Ile	Ser	Phe	Gln	His	Leu	His
				365					370					375
Arg	Leu	Thr	Cys	Leu	Lys	Leu	Trp	Tyr	Asn	His	Ile	Ala	Tyr	Ile
				380					385					390
Pro	Ile	Gln	Ile	Gly	Asn	Leu	Thr	Asn	Leu	Glu	Arg	Leu	Tyr	Leu
				395					400					405
Asn	Arg	Asn	Lys	Ile	Glu	Lys	Ile	Pro	Thr	Gln	Leu	Phe	Tyr	Cys
				410					415					420
Arg	Lys	Leu	Arg	Tyr	Leu	Asp	Leu	Ser	His	Asn	Asn	Leu	Thr	Phe
				425					430					435
Leu	Pro	Ala	Asp	Ile	Gly	Leu	Leu	Gln	Asn	Leu	Gln	Asn	Leu	Ala
				440					445					450
Ile	Thr	Ala	Asn	Arg	Ile	Glu	Thr	Leu	Pro	Pro	Glu	Leu	Phe	Gln
				455					460					465
Cys	Arg	Lys	Leu	Arg	Ala	Leu	His	Leu	Gly	Asn	Asn	Val	Leu	Gln
				470					475					480
Ser	Leu	Pro	Ser	Arg	Val	Gly	Glu	Leu	Thr	Asn	Leu	Thr	Gln	Ile
				485					490					495
Glu	Leu	Arg	Gly	Asn	Arg	Leu	Glu	Cys	Leu	Pro	Val	Glu	Leu	Gly
				500					505					510
Glu	Cys	Pro	Leu	Leu	Lys	Arg	Ser	Gly	Leu	Val	Val	Glu	Glu	Asp
				515					520					525
Leu	Phe	Asn	Thr	Leu	Pro	Pro	Glu	Val	Lys	Glu	Arg	Leu	Trp	Arg
				530					535					540
Ala	Asp	Lys	Glu	Gln	Ala									
				545										

&lt;210&gt; 251

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 251

caacaatgag ggcaccaagc 20

&lt;210&gt; 252

&lt;211&gt; 24

FOBT20-02E6060



<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 252

gatggctagg ttctggaggt tctg 24

<210> 253

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 253

caacctgcag gagattgacc tcaaggacaa caacctcaag accatcg 47

<210> 254

<211> 1650

<212> DNA

<213> Homo Sapien

<400> 254

gcctgttgct gatgctgccg tgcggtactt gtcattggagc tggcactgcg 50  
 gcgctctccc gtcccgcggg ggttgctgct gctgccgctg ctgctgggccc 100  
 tgaacgcagg agctgtcatt gactggccca cagaggaggg caaggaagta 150  
 tgggattatg tgacgggtccg caaggatgcc tacatgttct ggtggctcta 200  
 ttatgccacc aactcctgca agaacttctc agaactgccc ctggtcattg 250  
 ggcttcaggg cgggccaggc ggttctagca ctggatttgg aaactttgag 300  
 gaaattgggc cccttgacag tgatctcaaa ccacggaaaa ccacctggct 350  
 ccaggctgcc agtctcctat ttgtggataa tcccgtgggc actgggttca 400  
 gttatgtgaa tggtagtggt gcctatgcca aggacctggc tatggtggct 450  
 tcagacatga tggttctcct gaagaccttc ttcagttgcc acaaagaatt 500  
 ccagacagtt ccattctaca ttttctcaga gtccatgga ggaaaaatgg 550  
 cagctggcat tggctagag ctttataagg ccattcagcg agggaccatc 600  
 aagtgcaact ttgcgggggt tgccttgggt gattcctgga tctccctgt 650  
 tgattcgggt ctctcctggg gaccttacct gtacagcatg tctcttctcg 700

FOR 20-02E50550

aagacaaagg tctggcagag gtgtctaagg ttgcagagca agtactgaat 750  
gccgtaaata aggggctcta cagagaggcc acagagctgt gggggaaagc 800  
agaaatgatac attgaacaga acacagatgg ggtgaacttc tataacatct 850  
taactaaaag cactcccacg tctacaatgg agtcgagtct agaattcaca 900  
cagagccacc tagtttgtct ttgtcagcgc cactgagac acctacaacg 950  
agatgcctta agccagctca tgaatggccc catcagaaag aagctcaaaa 1000  
ttattcctga ggatcaatcc tggggaggcc aggctaccaa cgtctttgtg 1050  
aacatggagg aggacttcat gaagccagtc attagcattg tggacgagtt 1100  
gctggaggca gggatcaacg tgacggtgta taatggacag ctggatctca 1150  
tcgtagatac catgggtcag gaggcctggg tgcggaaact gaagtggcca 1200  
gaactgccta aattcagtc gctgaagtgg aaggccctgt acagtgaccc 1250  
taaattcttg gaaacatctg cttttgtcaa gtcttacaag aaccttgctt 1300  
tctactggat tctgaaagct ggtcatatgg ttcttctga ccaaggggac 1350  
atggctctga agatgatgag actggtgact cagcaagaat aggatggatg 1400  
gggctggaga tgagctgggt tggccttggg gcacagagct gagctgaggc 1450  
cgctgaagct gtaggaagcg ccattcttcc ctgtatctaa ctggggctgt 1500  
gatcaagaag gttctgacca gcttctgcag aggataaaat cattgtctct 1550  
ggaggcaatt tggaaattat ttctgcttct taaaaaaacc taagattttt 1600  
taaaaaattg atttgttttg atcaaaataa aggatgataa tagatattaa 1650

<210> 255

<211> 452

<212> PRT

<213> Homo Sapien

<400> 255

Met	Glu	Leu	Ala	Leu	Arg	Arg	Ser	Pro	Val	Pro	Arg	Trp	Leu	Leu
1				5					10				15	
Leu	Leu	Pro	Leu	Leu	Leu	Gly	Leu	Asn	Ala	Gly	Ala	Val	Ile	Asp
				20					25				30	
Trp	Pro	Thr	Glu	Glu	Gly	Lys	Glu	Val	Trp	Asp	Tyr	Val	Thr	Val
				35					40				45	

Arg	Lys	Asp	Ala	Tyr	Met	Phe	Trp	Trp	Leu	Tyr	Tyr	Ala	Thr	Asn
				50					55					60
Ser	Cys	Lys	Asn	Phe	Ser	Glu	Leu	Pro	Leu	Val	Met	Trp	Leu	Gln
				65					70					75
Gly	Gly	Pro	Gly	Gly	Ser	Ser	Thr	Gly	Phe	Gly	Asn	Phe	Glu	Glu
				80					85					90
Ile	Gly	Pro	Leu	Asp	Ser	Asp	Leu	Lys	Pro	Arg	Lys	Thr	Thr	Trp
				95					100					105
Leu	Gln	Ala	Ala	Ser	Leu	Leu	Phe	Val	Asp	Asn	Pro	Val	Gly	Thr
				110					115					120
Gly	Phe	Ser	Tyr	Val	Asn	Gly	Ser	Gly	Ala	Tyr	Ala	Lys	Asp	Leu
				125					130					135
Ala	Met	Val	Ala	Ser	Asp	Met	Met	Val	Leu	Leu	Lys	Thr	Phe	Phe
				140					145					150
Ser	Cys	His	Lys	Glu	Phe	Gln	Thr	Val	Pro	Phe	Tyr	Ile	Phe	Ser
				155					160					165
Glu	Ser	Tyr	Gly	Gly	Lys	Met	Ala	Ala	Gly	Ile	Gly	Leu	Glu	Leu
				170					175					180
Tyr	Lys	Ala	Ile	Gln	Arg	Gly	Thr	Ile	Lys	Cys	Asn	Phe	Ala	Gly
				185					190					195
Val	Ala	Leu	Gly	Asp	Ser	Trp	Ile	Ser	Pro	Val	Asp	Ser	Val	Leu
				200					205					210
Ser	Trp	Gly	Pro	Tyr	Leu	Tyr	Ser	Met	Ser	Leu	Leu	Glu	Asp	Lys
				215					220					225
Gly	Leu	Ala	Glu	Val	Ser	Lys	Val	Ala	Glu	Gln	Val	Leu	Asn	Ala
				230					235					240
Val	Asn	Lys	Gly	Leu	Tyr	Arg	Glu	Ala	Thr	Glu	Leu	Trp	Gly	Lys
				245					250					255
Ala	Glu	Met	Ile	Ile	Glu	Gln	Asn	Thr	Asp	Gly	Val	Asn	Phe	Tyr
				260					265					270
Asn	Ile	Leu	Thr	Lys	Ser	Thr	Pro	Thr	Ser	Thr	Met	Glu	Ser	Ser
				275					280					285
Leu	Glu	Phe	Thr	Gln	Ser	His	Leu	Val	Cys	Leu	Cys	Gln	Arg	His
				290					295					300
Val	Arg	His	Leu	Gln	Arg	Asp	Ala	Leu	Ser	Gln	Leu	Met	Asn	Gly

305	310	315
Pro Ile Arg Lys Lys Leu Lys Ile Ile	Pro Glu Asp Gln Ser Trp	
320	325	330
Gly Gly Gln Ala Thr Asn Val Phe Val	Asn Met Glu Glu Asp Phe	
335	340	345
Met Lys Pro Val Ile Ser Ile Val Asp	Glu Leu Leu Glu Ala Gly	
350	355	360
Ile Asn Val Thr Val Tyr Asn Gly Gln	Leu Asp Leu Ile Val Asp	
365	370	375
Thr Met Gly Gln Glu Ala Trp Val Arg	Lys Leu Lys Trp Pro Glu	
380	385	390
Leu Pro Lys Phe Ser Gln Leu Lys Trp	Lys Ala Leu Tyr Ser Asp	
395	400	405
Pro Lys Ser Leu Glu Thr Ser Ala Phe	Val Lys Ser Tyr Lys Asn	
410	415	420
Leu Ala Phe Tyr Trp Ile Leu Lys Ala	Gly His Met Val Pro Ser	
425	430	435
Asp Gln Gly Asp Met Ala Leu Lys Met	Met Arg Leu Val Thr Gln	
440	445	450

Gln Glu

&lt;210&gt; 256

&lt;211&gt; 1100

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 256

```

ggccgcggga gaggaggcca tgggcgcgcg cggggcgctg ctgctggcgc 50
tgctgctggc tcgggctgga ctcaggaagc cggagtcgca ggaggcggcg 100
ccgttatcag gaccatgcgg ccgacgggtc atcacgtcgc gcatcgtggg 150
tggagaggac gccgaactcg ggcgttggcc gtggcagggg agcctgcgcc 200
tgtgggattc ccacgtatgc ggagtgcgcc tgctcagcca ccgctgggca 250
ctcacggcgg cgcaactgctt tgaaacctat agtgacctta gtgatccctc 300
cgggtggatg gtccagtttg gccagctgac ttccatgcca tccttctgga 350
gcctgcaggc ctactacacc cgttacttcg tatcgaatat ctatctgagc 400

```

cctcgctacc tggggaattc accctatgac attgccttgg tgaagctgtc 450  
 tgcacctgtc acctacacta aacacatcca gcccatctgt ctccaggcct 500  
 ccacatttga gtttgagaac cggacagact gctgggtgac tggctggggg 550  
 tacatcaaag aggatgaggc actgccatct cccacacccc tccaggaagt 600  
 tcaggctgcc atcataaaca actctatgtg caaccacctc ttctcaagt 650  
 acagtttccg caaggacatc tttggagaca tggtttgtgc tggcaacgcc 700  
 caaggcggga aggatgcctg cttcggtgac tcagggtggac ccttggcctg 750  
 taacaagaat ggactgtggt atcagattgg agtcgtgagc tggggagtgg 800  
 gctgtggtcg gcccaatcgg ccggtgtct acaccaatat cagccaccac 850  
 tttgagtga tccagaagct gatggcccag agtggcatgt cccagccaga 900  
 cccctcctgg ccaactactct tttccctct tctctgggct ctcccactcc 950  
 tggggccggg ctgagcctac ctgagcccat gcagcctggg gccactgcca 1000  
 agtcaggccc tggttctctt ctgtcttggt tggtaataaa cacattccag 1050  
 ttgatgcctt gcagggcatt cttcaaaaaa aaaaaaaaaa aaaaaaaaaa 1100

<210> 257

<211> 314

<212> PRT

<213> Homo Sapien

<400> 257

Met	Gly	Ala	Arg	Gly	Ala	Leu	Leu	Leu	Ala	Leu	Leu	Leu	Ala	Arg
1				5					10					15

Ala	Gly	Leu	Arg	Lys	Pro	Glu	Ser	Gln	Glu	Ala	Ala	Pro	Leu	Ser
				20					25					30

Gly	Pro	Cys	Gly	Arg	Arg	Val	Ile	Thr	Ser	Arg	Ile	Val	Gly	Gly
				35					40					45

Glu	Asp	Ala	Glu	Leu	Gly	Arg	Trp	Pro	Trp	Gln	Gly	Ser	Leu	Arg
				50					55					60

Leu	Trp	Asp	Ser	His	Val	Cys	Gly	Val	Ser	Leu	Leu	Ser	His	Arg
				65					70					75

Trp	Ala	Leu	Thr	Ala	Ala	His	Cys	Phe	Glu	Thr	Tyr	Ser	Asp	Leu
				80					85					90

09909320.071801

Ser Asp Pro Ser Gly Trp Met Val Gln Phe Gly Gln Leu Thr Ser  
 95 100 105  
 Met Pro Ser Phe Trp Ser Leu Gln Ala Tyr Tyr Thr Arg Tyr Phe  
 110 115 120  
 Val Ser Asn Ile Tyr Leu Ser Pro Arg Tyr Leu Gly Asn Ser Pro  
 125 130 135  
 Tyr Asp Ile Ala Leu Val Lys Leu Ser Ala Pro Val Thr Tyr Thr  
 140 145 150  
 Lys His Ile Gln Pro Ile Cys Leu Gln Ala Ser Thr Phe Glu Phe  
 155 160 165  
 Glu Asn Arg Thr Asp Cys Trp Val Thr Gly Trp Gly Tyr Ile Lys  
 170 175 180  
 Glu Asp Glu Ala Leu Pro Ser Pro His Thr Leu Gln Glu Val Gln  
 185 190 195  
 Val Ala Ile Ile Asn Asn Ser Met Cys Asn His Leu Phe Leu Lys  
 200 205 210  
 Tyr Ser Phe Arg Lys Asp Ile Phe Gly Asp Met Val Cys Ala Gly  
 215 220 225  
 Asn Ala Gln Gly Gly Lys Asp Ala Cys Phe Gly Asp Ser Gly Gly  
 230 235 240  
 Pro Leu Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly Val  
 245 250 255  
 Val Ser Trp Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val  
 260 265 270  
 Tyr Thr Asn Ile Ser His His Phe Glu Trp Ile Gln Lys Leu Met  
 275 280 285  
 Ala Gln Ser Gly Met Ser Gln Pro Asp Pro Ser Trp Pro Leu Leu  
 290 295 300  
 Phe Phe Pro Leu Leu Trp Ala Leu Pro Leu Leu Gly Pro Val  
 305 310

&lt;210&gt; 258

&lt;211&gt; 2427

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 258

cccacgcgtc cgcggacgcg tgggaagggc agaatgggac tccaagcctg 50

cctcctaggg ctctttgccc tcatectctc tggcaaagtc agttacagcc 100  
 cggagcccga ccagcggagg acgctgcccc caggctgggt gtccctgggc 150  
 cgtgcggacc ctgaggaaga gctgagtctc acctttgccc tgagacagca 200  
 gaatgtggaa agactctcgg agctggtgca ggctgtgtcg gatccagct 250  
 ctctcaata cggaaaatac ctgaccctag agaatgtggc tgatctggtg 300  
 aggccatccc cactgaccct ccacacggtg caaaaatggc tcttggcagc 350  
 cggagcccag aagtgccatt ctgtgatcac acaggacttt ctgacttgct 400  
 ggctgagcat ccgacaagca gagctgctgc tccctggggc tgagtttcat 450  
 cactatgtgg gaggacctac ggaaacccat gttgtaaggc cccacatcc 500  
 ctaccagctt ccacaggcct tggcccccca tgtggacttt gtggggggac 550  
 tgcaccgttt tcccccaaca tcatccctga ggcaacgtcc tgagccgcag 600  
 gtgacaggga ctgtaggcct gcatctgggg gtaacccct ctgtgatccg 650  
 taagcgatac aacttgacct cacaagacgt gggctctggc accagcaata 700  
 acagccaagc ctgtgcccag ttccctggagc agtatttcca tgactcagac 750  
 ctggctcagt tcatgcgcct ctccggtggc aactttgcac atcaggcatc 800  
 agtagcccggt gtggttggac aacagggccg gggccgggcc gggattgagg 850  
 ccagtctaga tgtgcagtac ctgatgagtg ctggtgcca catctccacc 900  
 tgggtctaca gtagccctgg ccggcatgag ggacaggagc ccttctgca 950  
 gtggctcatg ctgctcagta atgagtcagc cctgccacat gtgcatactg 1000  
 tgagctatgg agatgatgag gactccctca gcagcgcta catccagcgg 1050  
 gtcaacactg agtcatgaa ggctgccgct cggggtctca cctgctctt 1100  
 cgcctcaggt gacagtgggg ccgggtgttg gtctgtctct ggaagacacc 1150  
 agttccgccc taccttccct gcctccagcc cctatgtcac cacagtggga 1200  
 ggcacatcct tccaggaacc ttctctcatc acaaatgaaa ttgttgacta 1250  
 tatcagtggg ggtggttca gcaatgtgtt cccacggcct tcataccagg 1300  
 aggaagctgt aacgaagttc ctgagctcta gccccacct gccaccatcc 1350  
 agttacttca atgccagtgg ccgtgcctac ccagatgtgg ctgcactttc 1400

09909320-071801

tgatggctac tgggtgggtca gcaacagagt gcccattcca tgggtgtccg 1450  
 gaacctcggc ctctactcca gtgtttgggg ggatcctatc cttgatcaat 1500  
 gagcacagga tccttagtgg ccgccccct cttggctttc tcaaccaag 1550  
 gctctaccag cagcatgggg caggtctctt tgatgtaacc cgtggctgcc 1600  
 atgagtcctg tctggatgaa gaggtagagg gccagggttt ctgctctggg 1650  
 cctggctggg atcctgtaac aggtcgggga acaccaactt cccagctttg 1700  
 ctgaagactc tactcaaccc ctgacctttt cctatcagga gagatggctt 1750  
 gtccccgcc ctgaagctgg cagttcagtc ccttattctg ccctgttgga 1800  
 agccctgctg aacctcaac tattgactgc tgcagacagc ttatctccct 1850  
 aacctgaaa tgetgtgagc ttgacttgac tcccaacctt accatgctcc 1900  
 atcatactca ggtctcccta ctctgcctt agattcctca ataagatgct 1950  
 gtaactagca ttttttgaat gcctctccct ccgcatctca tctttctctt 2000  
 ttcaatcagg cttttccaaa gggttgtata cagactctgt gcactatttc 2050  
 acttgatatt cattcccca ttcactgcaa ggagacctct actgtcaccg 2100  
 tttactcttt cctacctga catccagaaa caatggctc cagtgcatac 2150  
 ttctcaatct ttgctttatg gcctttccat catagttgcc cactccctct 2200  
 ccttacttag ctccaggtc ttaacttctc tgactactct tgtcttctc 2250  
 tctcatcaat ttctgcttct tcatggaatg ctgaccttca ttgctccatt 2300  
 tgtagatttt tgetcttctc agtttactca ttgtccctg gaacaaatca 2350  
 ctgacatcta caaccattac catctcacta aataagactt tctatccaat 2400  
 aatgattgat acctcaaag taaaaa 2427

<210> 259

<211> 556

<212> PRT

<213> Homo Sapien

<400> 259

Met	Gly	Leu	Gln	Ala	Cys	Leu	Leu	Gly	Leu	Phe	Ala	Leu	Ile	Leu
1					5				10					15

Ser Gly Lys Cys Ser Tyr Ser Pro Glu Pro Asp Gln Arg Arg Thr



	20		25		30
Leu Pro Pro Gly Trp Val Ser Leu Gly Arg Ala Asp Pro Glu Glu	35		40		45
Glu Leu Ser Leu Thr Phe Ala Leu Arg Gln Gln Asn Val Glu Arg	50		55		60
Leu Ser Glu Leu Val Gln Ala Val Ser Asp Pro Ser Ser Pro Gln	65		70		75
Tyr Gly Lys Tyr Leu Thr Leu Glu Asn Val Ala Asp Leu Val Arg	80		85		90
Pro Ser Pro Leu Thr Leu His Thr Val Gln Lys Trp Leu Leu Ala	95		100		105
Ala Gly Ala Gln Lys Cys His Ser Val Ile Thr Gln Asp Phe Leu	110		115		120
Thr Cys Trp Leu Ser Ile Arg Gln Ala Glu Leu Leu Leu Pro Gly	125		130		135
Ala Glu Phe His His Tyr Val Gly Gly Pro Thr Glu Thr His Val	140		145		150
Val Arg Ser Pro His Pro Tyr Gln Leu Pro Gln Ala Leu Ala Pro	155		160		165
His Val Asp Phe Val Gly Gly Leu His Arg Phe Pro Pro Thr Ser	170		175		180
Ser Leu Arg Gln Arg Pro Glu Pro Gln Val Thr Gly Thr Val Gly	185		190		195
Leu His Leu Gly Val Thr Pro Ser Val Ile Arg Lys Arg Tyr Asn	200		205		210
Leu Thr Ser Gln Asp Val Gly Ser Gly Thr Ser Asn Asn Ser Gln	215		220		225
Ala Cys Ala Gln Phe Leu Glu Gln Tyr Phe His Asp Ser Asp Leu	230		235		240
Ala Gln Phe Met Arg Leu Phe Gly Gly Asn Phe Ala His Gln Ala	245		250		255
Ser Val Ala Arg Val Val Gly Gln Gln Gly Arg Gly Arg Ala Gly	260		265		270
Ile Glu Ala Ser Leu Asp Val Gln Tyr Leu Met Ser Ala Gly Ala	275		280		285

09909320-071801

Asn Ile Ser Thr Trp Val Tyr Ser Ser Pro Gly Arg His Glu Gly	290	295	300
Gln Glu Pro Phe Leu Gln Trp Leu Met Leu Leu Ser Asn Glu Ser	305	310	315
Ala Leu Pro His Val His Thr Val Ser Tyr Gly Asp Asp Glu Asp	320	325	330
Ser Leu Ser Ser Ala Tyr Ile Gln Arg Val Asn Thr Glu Leu Met	335	340	345
Lys Ala Ala Ala Arg Gly Leu Thr Leu Leu Phe Ala Ser Gly Asp	350	355	360
Ser Gly Ala Gly Cys Trp Ser Val Ser Gly Arg His Gln Phe Arg	365	370	375
Pro Thr Phe Pro Ala Ser Ser Pro Tyr Val Thr Thr Val Gly Gly	380	385	390
Thr Ser Phe Gln Glu Pro Phe Leu Ile Thr Asn Glu Ile Val Asp	395	400	405
Tyr Ile Ser Gly Gly Gly Phe Ser Asn Val Phe Pro Arg Pro Ser	410	415	420
Tyr Gln Glu Glu Ala Val Thr Lys Phe Leu Ser Ser Ser Pro His	425	430	435
Leu Pro Pro Ser Ser Tyr Phe Asn Ala Ser Gly Arg Ala Tyr Pro	440	445	450
Asp Val Ala Ala Leu Ser Asp Gly Tyr Trp Val Val Ser Asn Arg	455	460	465
Val Pro Ile Pro Trp Val Ser Gly Thr Ser Ala Ser Thr Pro Val	470	475	480
Phe Gly Gly Ile Leu Ser Leu Ile Asn Glu His Arg Ile Leu Ser	485	490	495
Gly Arg Pro Pro Leu Gly Phe Leu Asn Pro Arg Leu Tyr Gln Gln	500	505	510
His Gly Ala Gly Leu Phe Asp Val Thr Arg Gly Cys His Glu Ser	515	520	525
Cys Leu Asp Glu Glu Val Glu Gly Gln Gly Phe Cys Ser Gly Pro	530	535	540
Gly Trp Asp Pro Val Thr Gly Trp Gly Thr Pro Thr Ser Gln Leu	545	550	555

FOI b7D b2E b6B b7C

Cys

&lt;210&gt; 260

&lt;211&gt; 1638

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 260

```

gccgcgcgct ctctcccggc gcccacacct gtctgagcgg cgcagcgagc 50
cgcggccccg gcgggctgct cggcgcggaa cagtgtctcg catggcaggg 100
attccagggc tctcttctct tctcttcttt ctgctctgtg ctggtgggca 150
agtgagccct tacagtgcc cctggaaacc cacttggcct gcataccgcc 200
tcctgtcgt cttgccccag tctacctca atttagccaa gccagacttt 250
ggagccgaag ccaaattaga agtatcttct tcatgtggac ccagtggtca 300
taagggaact cactgcccc cttacgaaga ggccaagcaa tatctgtctt 350
atgaaacgct ctatgccaat ggcagccgca cagagacgca ggtgggcatc 400
tacatcctca gcagtagtgg agatggggcc caacaccgag actcagggtc 450
ttcaggaaag tctcgaagga agcggcagat ttatggctat gacagcaggt 500
tcagcatttt tgggaaggac ttctgtctca actaccttt ctcaacatca 550
gtgaagtatt ccacgggctg caccggcacc ctggtggcag agaagcatgt 600
cctcacagct gccactgca tacacgatgg aaaaacctat gtgaaaggaa 650
cccagaagct tcgagtgggc ttctaaagc ccaagtttaa agatggtggt 700
cgaggggcca acgactccac ttcagccatg cccgagcaga tgaaatttca 750
gtggatccgg gtgaaacgca cccatgtgcc caagggttgg atcaagggca 800
atgccaatga catcggcctg gattatgatt atgcctcctt ggaactcaaa 850
aagccccaca agagaaaatt tatgaagatt ggggtgagcc ctctgtctaa 900
gcagctgcca gggggcagaa ttcacttctc tggttatgac aatgaccgac 950
caggcaattt ggtgtatcgc ttctgtgacg tcaaagacga gacctatgac 1000
ttgctctacc agcaatgcga tgcccagcca ggggccagcg ggtctggggg 1050
ctatgtgagg atgtggaaga gacagcagca gaagtgggag cgaaaaatta 1100

```

F03720.02E60650

ttggcatttt ttcagggcac cagtgggtgg acatgaatgg ttccccacag 1150  
 gatttcaacg tggctgtcag aatcactcct ctcaaataatg cccagatttg 1200  
 ctattggatt aaaggaaact acctggattg tagggagggg tgacacagtg 1250  
 ttccctcctg gcagcaatta aggggtcttca tgttcttatt ttaggagagg 1300  
 ccaaattggt ttttgtcatt ggcgtgcaca cgtgtgtgtg tgtgtgtgtg 1350  
 tgtgtgtaag gtgtcttata atcttttacc tatttcttac aattgcaaga 1400  
 tgactggctt tactatttga aaactgggtt gtgtatcata tcatatatca 1450  
 ttttaagcagt ttgaaggcat acttttgcag agaaataaaa aaaatactga 1500  
 tttggggcaa tgaggaatat ttgacaatta agttaatctt cacgtttttg 1550  
 caaactttga tttttatttc atctgaactt gtttcaaaga tttatattaa 1600  
 atatttggca tacaagagat atgaaaaaaaa aaaaaaaaa 1638

<210> 261

<211> 383

<212> PRT

<213> Homo Sapien

<400> 261

Met	Ala	Gly	Ile	Pro	Gly	Leu	Leu	Phe	Leu	Leu	Phe	Phe	Leu	Leu	1	5	10	15
Cys	Ala	Val	Gly	Gln	Val	Ser	Pro	Tyr	Ser	Ala	Pro	Trp	Lys	Pro	20	25	30	
Thr	Trp	Pro	Ala	Tyr	Arg	Leu	Pro	Val	Val	Leu	Pro	Gln	Ser	Thr	35	40	45	
Leu	Asn	Leu	Ala	Lys	Pro	Asp	Phe	Gly	Ala	Glu	Ala	Lys	Leu	Glu	50	55	60	
Val	Ser	Ser	Ser	Cys	Gly	Pro	Gln	Cys	His	Lys	Gly	Thr	Pro	Leu	65	70	75	
Pro	Thr	Tyr	Glu	Glu	Ala	Lys	Gln	Tyr	Leu	Ser	Tyr	Glu	Thr	Leu	80	85	90	
Tyr	Ala	Asn	Gly	Ser	Arg	Thr	Glu	Thr	Gln	Val	Gly	Ile	Tyr	Ile	95	100	105	
Leu	Ser	Ser	Ser	Gly	Asp	Gly	Ala	Gln	His	Arg	Asp	Ser	Gly	Ser	110	115	120	

09909320-071801

Ser Gly Lys Ser Arg Arg Lys Arg Gln Ile Tyr Gly Tyr Asp Ser	125	130	135
Arg Phe Ser Ile Phe Gly Lys Asp Phe Leu Leu Asn Tyr Pro Phe	140	145	150
Ser Thr Ser Val Lys Leu Ser Thr Gly Cys Thr Gly Thr Leu Val	155	160	165
Ala Glu Lys His Val Leu Thr Ala Ala His Cys Ile His Asp Gly	170	175	180
Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val Gly Phe Leu	185	190	195
Lys Pro Lys Phe Lys Asp Gly Gly Arg Gly Ala Asn Asp Ser Thr	200	205	210
Ser Ala Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg Val Lys	215	220	225
Arg Thr His Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp	230	235	240
Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro	245	250	255
His Lys Arg Lys Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys	260	265	270
Gln Leu Pro Gly Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp	275	280	285
Arg Pro Gly Asn Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu	290	295	300
Thr Tyr Asp Leu Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala	305	310	315
Ser Gly Ser Gly Val Tyr Val Arg Met Trp Lys Arg Gln Gln Gln	320	325	330
Lys Trp Glu Arg Lys Ile Ile Gly Ile Phe Ser Gly His Gln Trp	335	340	345
Val Asp Met Asn Gly Ser Pro Gln Asp Phe Asn Val Ala Val Arg	350	355	360
Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Tyr Trp Ile Lys Gly	365	370	375
Asn Tyr Leu Asp Cys Arg Glu Gly	380		

09909320.071801

<210> 262  
 <211> 1378  
 <212> DNA  
 <213> Homo Sapien

<400> 262  
 gcatgcacct ggggtctctcg agcctgctgc ctgctcccc gccccaccag 50  
 ccatgggtgggt ttctggagcg cccccagccc tgggtggggg ctgtctcggc 100  
 accttcacct cctgctgct gctggcgctg acagccatcc tcaatgcggc 150  
 caggatacct gttccccag cctgtgggaa gccccagcag ctgaaccggg 200  
 ttgtggggcg cgaggacagc actgacagcg agtggccctg gatcgtgagc 250  
 atccagaaga atgggaccca ccaactgcgc ggttctctgc tcaccagccg 300  
 ctgggtgatc actgctgccc actgtttcaa ggacaacctg aacaaacct 350  
 acctgttctc tgtgctgctg ggggcctggc agctggggaa cctggctct 400  
 cgggtccaga aggtgggtgt tgccctgggtg gagccccacc ctgtgtattc 450  
 ctggaaggaa ggtgcctgtg cagacattgc cctggtgcgt ctgcagcgct 500  
 ccatacagtt ctgcagagcg gtccctgcca tctgcctacc tgatgcctct 550  
 atccacctcc ctccaaacac ccaactgctg atctcaggct gggggagcat 600  
 ccaagatgga gttcccttgc cccacctca gacctgcag aagctgaagg 650  
 ttctatcat cgactcgga gtctgcagcc atctgtactg gcggggagca 700  
 ggacagggac ccatcactga ggacatgctg tgtgccggct acttgagggg 750  
 ggagcgggat gcttgtctgg gcgactccgg gggccccctc atgtgccagg 800  
 tggacggcgc ctggctgctg gccggcatca tcagctgggg cgagggctgt 850  
 gccgagcgca acaggcccg ggtctacatc agcctctctg cgcaccgctc 900  
 ctgggtggag aagatcgtgc aaggggtgca gctccgcggg cgcgctcagg 950  
 ggggtggggc cctcagggca ccgagccagg gctctggggc cgccgcgcgc 1000  
 tcctagggcg cagcgggacg cggggctcgg atctgaaagg cggccagatc 1050  
 cacatctgga tctggatctg cggcggcctc gggcggtttc ccccgccgta 1100  
 aataggctca tctacctcta cctctggggg cccggacggc tgctgcggaa 1150

103120"02E60660

aggaaacccc ctccccgacc cgccccgacgg cctcaggccc cctccaagg 1200  
 catcaggccc cgcccaacgg cctcatgtcc ccgccccac gacttccggc 1250  
 cccgcccccg ggccccagcg cttttgtgta tataaatggt aatgattttt 1300  
 ataggtattt gtaaccctgc ccacatatct tatttattcc tccaatttca 1350  
 ataaattatt tattctccaa aaaaaaaaa 1378

<210> 263

<211> 317

<212> PRT

<213> Homo Sapien.

<400> 263

Met	Val	Val	Ser	Gly	Ala	Pro	Pro	Ala	Leu	Gly	Gly	Gly	Cys	Leu	1	5	10	15
Gly	Thr	Phe	Thr	Ser	Leu	Leu	Leu	Leu	Ala	Ser	Thr	Ala	Ile	Leu	20	25	30	
Asn	Ala	Ala	Arg	Ile	Pro	Val	Pro	Pro	Ala	Cys	Gly	Lys	Pro	Gln	35	40	45	
Gln	Leu	Asn	Arg	Val	Val	Gly	Gly	Glu	Asp	Ser	Thr	Asp	Ser	Glu	50	55	60	
Trp	Pro	Trp	Ile	Val	Ser	Ile	Gln	Lys	Asn	Gly	Thr	His	His	Cys	65	70	75	
Ala	Gly	Ser	Leu	Leu	Thr	Ser	Arg	Trp	Val	Ile	Thr	Ala	Ala	His	80	85	90	
Cys	Phe	Lys	Asp	Asn	Leu	Asn	Lys	Pro	Tyr	Leu	Phe	Ser	Val	Leu	95	100	105	
Leu	Gly	Ala	Trp	Gln	Leu	Gly	Asn	Pro	Gly	Ser	Arg	Ser	Gln	Lys	110	115	120	
Val	Gly	Val	Ala	Trp	Val	Glu	Pro	His	Pro	Val	Tyr	Ser	Trp	Lys	125	130	135	
Glu	Gly	Ala	Cys	Ala	Asp	Ile	Ala	Leu	Val	Arg	Leu	Glu	Arg	Ser	140	145	150	
Ile	Gln	Phe	Ser	Glu	Arg	Val	Leu	Pro	Ile	Cys	Leu	Pro	Asp	Ala	155	160	165	
Ser	Ile	His	Leu	Pro	Pro	Asn	Thr	His	Cys	Trp	Ile	Ser	Gly	Trp	170	175	180	

09909320.074801





0963 R070716L

<400> 270  
gcacctgtca cctacactaa acacatccag cccatctgtc tccaggcctc 50

<210> 271  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 271  
gcggaagggc agaatgggac tccaag 26

<210> 272  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 272  
cagccctgcc acatgtgc 18

<210> 273  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 273  
tactgggtgg tcagcaac 18

<210> 274  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 274  
ggcgaagagc agggtgagac cccg 24

<210> 275  
<211> 45

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

FOBT40-02E60660

<400> 275  
gccctcatcc tctctggcaa atgcagttac agcccggagc ccgac 45

<210> 276

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 276

gggcagggat tccagggctc c 21

<210> 277

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 277

ggctatgaca gcaggttc 18

<210> 278

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 278

tgacaatgac cgaccagg 18

<210> 279

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 279

gcatcgcatt gctggtagag caag 24

<210> 280

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

FOR "Q" DEE60660

ccgctactgc tactgctggt ggccaccaca ggccccgttg gagccctcac 100

agatgaggag aaacgtttga tggtagagct gcacaacctc taccggggccc 150  
 aggtatcccc gacggcctca gacatgctgc acatgagatg ggacgaggag 200  
 ctggccgcct tcgccaaggc ctacgcacgg cagtgcgtgt ggggccacaa 250  
 caaggagcgc gggcgccgcg gcgagaatct gttcgccatc acagacgagg 300  
 gcatggacgt gccgctggcc atggaggagt ggcaccacga gcgtgagcac 350  
 tacaacctca gcgccgccac ctgcagccca ggccagatgt gcggccacta 400  
 caccgaggtg gtatgggcca agacagagag gatcggctgt ggttcccact 450  
 tctgtgagaa gctccagggt gttgaggaga ccaacatcga attactggtg 500  
 tgcaactatg agcctccggg gaacgtgaag gggaaacggc cctaccagga 550  
 ggggactccg tgctcccaat gtccctctgg ctaccactgc aagaactccc 600  
 tctgtgaacc catcggaagc ccggaagatg ctccaggattt gccttacctg 650  
 gtaactgagg ccccatcctt ccgggcgact gaagcatcag actctaggaa 700  
 aatgggtact cctttctccc tagcaacggg gattccggct ttcttggtaa 750  
 cagaggtctc aggctccctg gcaaccaagg ctctgcctgc tgtggaaacc 800  
 caggccccaa cttccttagc aacgaaagac ccgccctcca tggcaacaga 850  
 ggctccacct tgcgtaacaa ctgagggtccc ttccattttg gcagctcaca 900  
 gcctgcctc cttggatgag gagccagtta ccttccccaa atcgacccat 950  
 gttcctatcc caaaatcagc agacaaagtg acagacaaaa caaaagtgcc 1000  
 ctctaggagc ccagagaact ctctggaccc caagatgtcc ctgacagggg 1050  
 caagggaact cctaccccat gcccaggagg aggctgaggc tgaggctgag 1100  
 ttgcctcctt ccagttaggt cttggcctca gtttttccag cccaggacaa 1150  
 gccaggtgag ctgcaggcca cactggacca cacggggcac acctcctcca 1200  
 agtccctgcc caatttcccc aatacctctg ccaccgctaa tgccacgggt 1250  
 gggcgtgcc tggctctgca gtgcctctg ccagggtcag agggccctga 1300  
 caagcctagc gttgtgtcag ggctgaactc gggccctggc catgtgtggg 1350  
 gccctctcct gggactactg ctctgcctc ctctggtgtt ggctggaatc 1400

0909320.071301

ttctgaatgg gataccactc aaagggtgaa gaggtcagct gtcctcctgt 1450  
 catcttcccc accctgtccc cagcccctaa acaagatact tcttggttaa 1500  
 ggccctccgg aagggaaagg ctacggggca tgtgcctcat cacaccatcc 1550  
 atcctggagg cacaaggcct ggctggctgc gagctcagga ggccgcctga 1600  
 ggactgcaca ccggggccac acctctcctg cccctccctc ctgagtcctg 1650  
 ggggtgggag gatttgaggg agctcactgc ctacctggcc tggggctgtc 1700  
 tgccacacaca gcatgtgcgc tctccctgag tgctgtgta gctggggatg 1750  
 gggattccta ggggcagatg aaggacaagc cccactggag tggggttctt 1800  
 tgagtggggg aggcaggagc gagggaagga aagtaactcc tgactctcca 1850  
 ataaaaacct gtccaacctg tgaaa 1875

<210> 285

<211> 463

<212> PRT

<213> Homo Sapien

<400> 285

Met	His	Gly	Ser	Cys	Ser	Phe	Leu	Met	Leu	Leu	Leu	Pro	Leu	Leu					
1				5					10					15					
Leu	Leu	Leu	Val	Ala	Thr	Thr	Gly	Pro	Val	Gly	Ala	Leu	Thr	Asp					
				20					25					30					
Glu	Glu	Lys	Arg	Leu	Met	Val	Glu	Leu	His	Asn	Leu	Tyr	Arg	Ala					
				35					40					45					
Gln	Val	Ser	Pro	Thr	Ala	Ser	Asp	Met	Leu	His	Met	Arg	Trp	Asp					
				50					55					60					
Glu	Glu	Leu	Ala	Ala	Phe	Ala	Lys	Ala	Tyr	Ala	Arg	Gln	Cys	Val					
				65					70					75					
Trp	Gly	His	Asn	Lys	Glu	Arg	Gly	Arg	Arg	Gly	Glu	Asn	Leu	Phe					
				80					85					90					
Ala	Ile	Thr	Asp	Glu	Gly	Met	Asp	Val	Pro	Leu	Ala	Met	Glu	Glu					
				95					100					105					
Trp	His	His	Glu	Arg	Glu	His	Tyr	Asn	Leu	Ser	Ala	Ala	Thr	Cys					
				110					115					120					
Ser	Pro	Gly	Gln	Met	Cys	Gly	His	Tyr	Thr	Gln	Val	Val	Trp	Ala					
				125					130					135					

FOBT20-071801

Lys	Thr	Glu	Arg	Ile	Gly	Cys	Gly	Ser	His	Phe	Cys	Glu	Lys	Leu
				140					145					150
Gln	Gly	Val	Glu	Glu	Thr	Asn	Ile	Glu	Leu	Leu	Val	Cys	Asn	Tyr
				155					160					165
Glu	Pro	Pro	Gly	Asn	Val	Lys	Gly	Lys	Arg	Pro	Tyr	Gln	Glu	Gly
				170					175					180
Thr	Pro	Cys	Ser	Gln	Cys	Pro	Ser	Gly	Tyr	His	Cys	Lys	Asn	Ser
				185					190					195
Leu	Cys	Glu	Pro	Ile	Gly	Ser	Pro	Glu	Asp	Ala	Gln	Asp	Leu	Pro
				200					205					210
Tyr	Leu	Val	Thr	Glu	Ala	Pro	Ser	Phe	Arg	Ala	Thr	Glu	Ala	Ser
				215					220					225
Asp	Ser	Arg	Lys	Met	Gly	Thr	Pro	Ser	Ser	Leu	Ala	Thr	Gly	Ile
				230					235					240
Pro	Ala	Phe	Leu	Val	Thr	Glu	Val	Ser	Gly	Ser	Leu	Ala	Thr	Lys
				245					250					255
Ala	Leu	Pro	Ala	Val	Glu	Thr	Gln	Ala	Pro	Thr	Ser	Leu	Ala	Thr
				260					265					270
Lys	Asp	Pro	Pro	Ser	Met	Ala	Thr	Glu	Ala	Pro	Pro	Cys	Val	Thr
				275					280					285
Thr	Glu	Val	Pro	Ser	Ile	Leu	Ala	Ala	His	Ser	Leu	Pro	Ser	Leu
				290					295					300
Asp	Glu	Glu	Pro	Val	Thr	Phe	Pro	Lys	Ser	Thr	His	Val	Pro	Ile
				305					310					315
Pro	Lys	Ser	Ala	Asp	Lys	Val	Thr	Asp	Lys	Thr	Lys	Val	Pro	Ser
				320					325					330
Arg	Ser	Pro	Glu	Asn	Ser	Leu	Asp	Pro	Lys	Met	Ser	Leu	Thr	Gly
				335					340					345
Ala	Arg	Glu	Leu	Leu	Pro	His	Ala	Gln	Glu	Glu	Ala	Glu	Ala	Glu
				350					355					360
Ala	Glu	Leu	Pro	Pro	Ser	Ser	Glu	Val	Leu	Ala	Ser	Val	Phe	Pro
				365					370					375
Ala	Gln	Asp	Lys	Pro	Gly	Glu	Leu	Gln	Ala	Thr	Leu	Asp	His	Thr
				380					385					390
Gly	His	Thr	Ser	Ser	Lys	Ser	Leu	Pro	Asn	Phe	Pro	Asn	Thr	Ser
				395					400					405

Ala Thr Ala Asn Ala Thr Gly Gly Arg Ala Leu Ala Leu Gln Ser  
 410 415 420

Ser Leu Pro Gly Ala Glu Gly Pro Asp Lys Pro Ser Val Val Ser  
 425 430 435

Gly Leu Asn Ser Gly Pro Gly His Val Trp Gly Pro Leu Leu Gly  
 440 445 450

Leu Leu Leu Leu Pro Pro Leu Val Leu Ala Gly Ile Phe  
 455 460

<210> 286

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 286

tcctgcagtt tcctgatgc 19

<210> 287

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 287

ctcatattgc acaccagtaa ttcg 24

<210> 288

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 288

atgaggagaa acgtttgatg gtggagctgc acaacctcta ccggg 45

<210> 289

<211> 3662

<212> DNA

<213> Homo Sapien

<400> 289

gtaactgaag tcaggctttt catttgggaa gccccctcaa cagaattcgg 50

099320-02E50550



tcattctcca agttatggtg gacgtacttc tgttgttctc cctctgcttg 100  
 ctttttcaca ttagcagacc ggacttaagt cacaacagat tatctttcat 150  
 caaggcaagt tccatgagcc accttcaaag ccttcgagaa gtgaaactga 200  
 acaacaatga attggagacc attccaaatc tgggaccagt ctcggaat 250  
 attacacttc tctccttggc tggaaacagg attgttgaaa tactccctga 300  
 acatctgaaa gagtttcagt cccttgaaac tttggacctt agcagcaaca 350  
 atatttcaga gctccaaact gcatttccag ccctacagct caaatatctg 400  
 tatctcaaca gcaaccgagt cacatcaatg gaacctgggt attttgacaa 450  
 tttggccaac acactccttg tgtaaagct gaacaggaac cgaatctcag 500  
 ctatcccacc caagatgttt aaactgcccc aactgcaaca tctcgaattg 550  
 aaccgaaaca agattaaaaa tgtagatgga ctgacattcc aaggccttgg 600  
 tgctctgaag tctctgaaaa tgcaaagaaa tggagtaacg aaacttatgg 650  
 atggagcttt ttgggggctg agcaacatgg aaattttgca gctggaccat 700  
 aacaaccta cagagattac caaaggctgg ctttacggct tgctgatgct 750  
 gcaggaaactt catctcagcc aaaatgccat caacaggatc agccctgatg 800  
 cctgggagtt ctgccagaag ctcagtgagc tggacctaac tttcaatcac 850  
 ttatcaagggt tagatgattc aagcttcctt ggcctaagct tactaaatac 900  
 actgcacatt gggaaacaaca gagtcagcta cattgctgat tgtgccttcc 950  
 gggggctttc cagtttaaag actttggatc tgaagaacaa tgaaatttcc 1000  
 tggactattg aagacatgaa tgggtgctttc tctgggcttg acaaactgag 1050  
 gcgactgata ctccaaggaa atcggatccg ttctattact aaaaaagcct 1100  
 tcaactggttt ggatgcattg gagcatctag acctgagtga caacgcaatc 1150  
 atgtctttac aaggcaatgc attttcacaa atgaagaaac tgcaacaatt 1200  
 gcattttaat acatcaagcc ttttgtgcca ttgccagcta aaatggctcc 1250  
 cacagtgggt ggcggaaaac aactttcaga gctttgtaaa tgccagttgt 1300  
 gcccatcctc agctgctaaa aggaagaagc atttttgctg ttagcccaga 1350

tggctttgtg tgtgatgatt ttcccaaacc ccagatcacg gttcagccag 1400  
 aaacacagtc ggcaataaaa ggttccaatt tgagtttcat ctgctcagct 1450  
 gccagcagca gtgattcccc aatgactttt gcttggaata aagacaatga 1500  
 actactgcat gatgctgaaa tggaaaatta tgcacacctc cgggccaag 1550  
 gtggcgaggt gatggagtat accaccatcc ttgggtgctg cgaggtggaa 1600  
 ttgcccagtg aggggaaata tcagtgtgtc atctccaatc actttgggtc 1650  
 atcctactct gtcaaagcca agcttacagt aaatatgctt ccctcattca 1700  
 ccaagacccc catggatctc accatccgag ctggggccat ggcacgcttg 1750  
 gagtgtgctg ctgtggggca cccagccccc cagatagcct ggcagaagga 1800  
 tgggggcaca gacttcccag ctgcacggga gagacgcatg catgtgatgc 1850  
 ccgaggatga cgtgttcttt atcgtggatg tgaagataga ggacattggg 1900  
 gtatacagct gcacagctca gaacagtga ggaagtattt cagcaaagtc 1950  
 aactctgact gtctagaaa caccatcatt ttgcgggcca ctgttggacc 2000  
 gaactgtaac caaggagaa acagccgtcc tacagtgcac tgctggagga 2050  
 agccctcccc ctaaactgaa ctggaccaa gatgatagcc cattggtggt 2100  
 aaccgagagg cacttttttg cagcaggcaa tcagcttctg attattgtgg 2150  
 actcagatgt cagtgatgct gggaaataga catgtgagat gtctaacc 2200  
 cttggcactg agagaggaaa cgtgcgctc agtgtgatcc cactccaac 2250  
 ctgcgactcc cctcagatga cagcccatc gttagacgat gacggatggg 2300  
 ccactgtggg tgctgtgatc atagccgtgg ttgctgtgt ggtgggcacg 2350  
 tcactcgtgt ggggtggtcat catataccac acaaggcgga ggaatgaaga 2400  
 ttgcagcatt accaacacag atgagaccaa cttgccagca gatattccta 2450  
 gttatttgtc atctcaggga acgttagctg acaggcagga tgggtacgtg 2500  
 tcttcagaaa gtggaagcca ccaccagttt gtcacatctt caggtgctgg 2550  
 atttttctta ccacaacatg acagtagtgg gacctgcat attgacaata 2600  
 gcagtgaagc tgatgtggaa gctgccacag atctgttctt ttgtccgttt 2650  
 ttgggatcca caggccctat gtatttgaag ggaaatgtgt atggctcaga 2700

tccttttgaa acatatcata caggttgcag tcctgaccca agaacagttt 2750  
 taatggacca ctatgagccc agttacataa agaaaaagga gtgctaccca 2800  
 tgtttctcatc cttcagaaga atcctgcgaa cggagcttca gtaatatatc 2850  
 gtggccttca catgtgagga agctacttaa cactagttac tctcacaatg 2900  
 aaggacctgg aatgaaaaat ctgtgtctaa acaagtcctc ttttagatttt 2950  
 agtgcaaate cagagccagc gtcggttgcc tcgagtaatt ctttcatggg 3000  
 tacctttgga aaagctctca ggagacctca cctagatgcc tattcaagct 3050  
 ttggacagcc atcagattgt cagccaagag ccttttattt gaaagctcat 3100  
 tcttccccag acttggaactc tgggtcagag gaagatggga aagaaaggac 3150  
 agattttcag gaagaaaatc acatttgtac ctttaaacag actttagaaa 3200  
 actacaggac tccaaatttt cagtcttatg acttggaacac atagactgaa 3250  
 tgagacccaaa ggaaaagctt aacatactac ctcaagtga cttttattta 3300  
 aaagagagag aatcttatgt tttttaaatg gagttatgaa ttttaaaagg 3350  
 ataaaaatgc tttatttata cagatgaacc aaaattacaa aaagttatga 3400  
 aaatttttat actgggaatg atgctcatat aagaatacct ttttaaacta 3450  
 ttttttaact ttgttttatg caaaaaagta tcttacgtaa attaatagata 3500  
 taaatcatga ttattttatg tatttttata atgccagatt tctttttatg 3550  
 gaaaatgagt tactaaagca ttttaaataa tacctgcctt gtaccatttt 3600  
 ttaaatagaa gttacttcat tatattttgc acattatatt taataaaatg 3650  
 tgtcaatttg aa 3662

<210> 290

<211> 1059

<212> PRT

<213> Homo Sapien

<400> 290

Met	Val	Asp	Val	Leu	Leu	Leu	Phe	Ser	Leu	Cys	Leu	Leu	Phe	His
1				5					10				15	

Ile	Ser	Arg	Pro	Asp	Leu	Ser	His	Asn	Arg	Leu	Ser	Phe	Ile	Lys
				20					25					30

0909320.071801

Ala	Ser	Ser	Met	Ser	His	Leu	Gln	Ser	Leu	Arg	Glu	Val	Lys	Leu	35	40	45
Asn	Asn	Asn	Glu	Leu	Glu	Thr	Ile	Pro	Asn	Leu	Gly	Pro	Val	Ser	50	55	60
Ala	Asn	Ile	Thr	Leu	Leu	Ser	Leu	Ala	Gly	Asn	Arg	Ile	Val	Glu	65	70	75
Ile	Leu	Pro	Glu	His	Leu	Lys	Glu	Phe	Gln	Ser	Leu	Glu	Thr	Leu	80	85	90
Asp	Leu	Ser	Ser	Asn	Asn	Ile	Ser	Glu	Leu	Gln	Thr	Ala	Phe	Pro	95	100	105
Ala	Leu	Gln	Leu	Lys	Tyr	Leu	Tyr	Leu	Asn	Ser	Asn	Arg	Val	Thr	110	115	120
Ser	Met	Glu	Pro	Gly	Tyr	Phe	Asp	Asn	Leu	Ala	Asn	Thr	Leu	Leu	125	130	135
Val	Leu	Lys	Leu	Asn	Arg	Asn	Arg	Ile	Ser	Ala	Ile	Pro	Pro	Lys	140	145	150
Met	Phe	Lys	Leu	Pro	Gln	Leu	Gln	His	Leu	Glu	Leu	Asn	Arg	Asn	155	160	165
Lys	Ile	Lys	Asn	Val	Asp	Gly	Leu	Thr	Phe	Gln	Gly	Leu	Gly	Ala	170	175	180
Leu	Lys	Ser	Leu	Lys	Met	Gln	Arg	Asn	Gly	Val	Thr	Lys	Leu	Met	185	190	195
Asp	Gly	Ala	Phe	Trp	Gly	Leu	Ser	Asn	Met	Glu	Ile	Leu	Gln	Leu	200	205	210
Asp	His	Asn	Asn	Leu	Thr	Glu	Ile	Thr	Lys	Gly	Trp	Leu	Tyr	Gly	215	220	225
Leu	Leu	Met	Leu	Gln	Glu	Leu	His	Leu	Ser	Gln	Asn	Ala	Ile	Asn	230	235	240
Arg	Ile	Ser	Pro	Asp	Ala	Trp	Glu	Phe	Cys	Gln	Lys	Leu	Ser	Glu	245	250	255
Leu	Asp	Leu	Thr	Phe	Asn	His	Leu	Ser	Arg	Leu	Asp	Asp	Ser	Ser	260	265	270
Phe	Leu	Gly	Leu	Ser	Leu	Leu	Asn	Thr	Leu	His	Ile	Gly	Asn	Asn	275	280	285
Arg	Val	Ser	Tyr	Ile	Ala	Asp	Cys	Ala	Phe	Arg	Gly	Leu	Ser	Ser			

09909320-071801

	290		295		300
Leu Lys Thr Leu Asp Leu Lys Asn Asn Glu Ile Ser Trp Thr Ile	305		310		315
Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg	320		325		330
Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala	335		340		345
Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn	350		355		360
Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys	365		370		375
Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys	380		385		390
Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln	395		400		405
Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly	410		415		420
Arg Ser Ile Phe Ala Val Ser Pro Asp Gly Phe Val Cys Asp Asp	425		430		435
Phe Pro Lys Pro Gln Ile Thr Val Gln Pro Glu Thr Gln Ser Ala	440		445		450
Ile Lys Gly Ser Asn Leu Ser Phe Ile Cys Ser Ala Ala Ser Ser	455		460		465
Ser Asp Ser Pro Met Thr Phe Ala Trp Lys Lys Asp Asn Glu Leu	470		475		480
Leu His Asp Ala Glu Met Glu Asn Tyr Ala His Leu Arg Ala Gln	485		490		495
Gly Gly Glu Val Met Glu Tyr Thr Thr Ile Leu Arg Leu Arg Glu	500		505		510
Val Glu Phe Ala Ser Glu Gly Lys Tyr Gln Cys Val Ile Ser Asn	515		520		525
His Phe Gly Ser Ser Tyr Ser Val Lys Ala Lys Leu Thr Val Asn	530		535		540
Met Leu Pro Ser Phe Thr Lys Thr Pro Met Asp Leu Thr Ile Arg	545		550		555

T03T20"02E60660

Ala Gly Ala Met	Ala Arg Leu Glu Cys	Ala Ala Val Gly His	Pro
560		565	570
Ala Pro Gln Ile	Ala Trp Gln Lys Asp	Gly Gly Thr Asp Phe	Pro
575		580	585
Ala Ala Arg Glu	Arg Arg Met His Val	Met Pro Glu Asp Asp	Val
590		595	600
Phe Phe Ile Val	Asp Val Lys Ile Glu	Asp Ile Gly Val Tyr	Ser
605		610	615
Cys Thr Ala Gln	Asn Ser Ala Gly Ser	Ile Ser Ala Asn Ala	Thr
620		625	630
Leu Thr Val Leu	Glu Thr Pro Ser Phe	Leu Arg Pro Leu Leu	Asp
635		640	645
Arg Thr Val Thr	Lys Gly Glu Thr Ala	Val Leu Gln Cys Ile	Ala
650		655	660
Gly Gly Ser Pro	Pro Pro Lys Leu Asn	Trp Thr Lys Asp Asp	Ser
665		670	675
Pro Leu Val Val	Thr Glu Arg His Phe	Phe Ala Ala Gly Asn	Gln
680		685	690
Leu Leu Ile Ile	Val Asp Ser Asp Val	Ser Asp Ala Gly Lys	Tyr
695		700	705
Thr Cys Glu Met	Ser Asn Thr Leu Gly	Thr Glu Arg Gly Asn	Val
710		715	720
Arg Leu Ser Val	Ile Pro Thr Pro Thr	Cys Asp Ser Pro Gln	Met
725		730	735
Thr Ala Pro Ser	Leu Asp Asp Asp Gly	Trp Ala Thr Val Gly	Val
740		745	750
Val Ile Ile Ala	Val Val Cys Cys Val	Val Gly Thr Ser Leu	Val
755		760	765
Trp Val Val Ile	Ile Tyr His Thr Arg	Arg Arg Asn Glu Asp	Cys
770		775	780
Ser Ile Thr Asn	Thr Asp Glu Thr Asn	Leu Pro Ala Asp Ile	Pro
785		790	795
Ser Tyr Leu Ser	Ser Gln Gly Thr Leu	Ala Asp Arg Gln Asp	Gly
800		805	810

09909320-071301

Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser  
 815 820 825  
 Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr  
 830 835 840  
 Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr  
 845 850 855  
 Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr  
 860 865 870  
 Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His  
 875 880 885  
 Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr  
 890 895 900  
 Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His  
 905 910 915  
 Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp  
 920 925 930  
 Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn  
 935 940 945  
 Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu  
 950 955 960  
 Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn  
 965 970 975  
 Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu  
 980 985 990  
 Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg  
 995 1000 1005  
 Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly  
 1010 1015 1020  
 Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn  
 1025 1030 1035  
 His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro  
 1040 1045 1050  
 Asn Phe Gln Ser Tyr Asp Leu Asp Thr  
 1055

&lt;210&gt; 291

&lt;211&gt; 2906

T08F20"02E60660

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 291

```

ggggagagga attgaccatg taaaaggaga cttttttttt tgggtggtggt 50
ggctgttggg tgccttgcaa aaatgaagga tgcaggacgc agctttctcc 100
tgaaccgaa cgcaatggat aaactgattg tgcaagagag aaggaagaac 150
gaagcttttt cttgtgagcc ctggatctta acacaaatgt gtatatgtgc 200
acacagggag cattcaagaa tgaaataaac cagagttaga cccgcggggg 250
ttggtgtggt ctgacataaa taaataatct taaagcagct gttccccctcc 300
ccacccccaa aaaaaaggat gattggaaat gaagaaccga ggattcacia 350
agaaaaaagt atgttcattt ttctctataa aggagaaagt gagccaagga 400
gatatttttg gaatgaaaag tttggggctt ttttagtaaa gtaaagaact 450
ggtgtggtgg tgttttcctt tctttttgaa tttcccacia gaggagagga 500
aattaataat acatctgcaa agaaatttca gagaagaaaa gttgaccgag 550
gcagattgag gcattgattg ggggagagaa accagcagag cacagttgga 600
tttgtgcta tggtgactaa aattgacgga taattgcagt tggatttttc 650
ttcatcaacc tccttttttt taaattttta ttcccttttg tatcaagatc 700
atgcgttttc tcttggtctt aaccacctgg atttccatct ggatgttgct 750
gtgatcagtc tgaaatacaa ctgtttgaat tccagaagga ccaacaccag 800
ataaattatg aatgttgaac aagatgacct tacatccaca gcagataatg 850
ataggtccta ggtttaacag ggccctatct gacccctgc ttgtggtgct 900
gctggctctt caacttcttg tgggtggtgg tctggtgagg gctcagacct 950
gcccttctgt gtgctcctgc agcaaccagt tcagcaaggt gatttgtggt 1000
cggaaaaacc tgcgtgaggt tccggatggc atctccacca acacacggct 1050
gctgaacctc catgagaacc aaatccagat catcaaagtg aacagcttca 1100
agcattgag gcacttgaa atcctacagt tgagtaggaa ccatatcaga 1150
accattgaaa ttggggcttt caatggtctg gcgaacctca acactctgga 1200
actctttgac aatcgtctta ctaccatccc gaatggagct tttgtatact 1250

```



09503E070301

catggaaagc cacctgcccc tgctgtctat cgagcatgag cacctaaatc 2600  
 actataactc atacaaatct cccttcaacc acacaacaac agttaacaca 2650  
 ataaattcaa tacacagttc agtgcattgaa ccgttattga tccgaatgaa 2700  
 ctctaaagac aatgtacaag agactcaaatt ctaaaacatt tacagagtta 2750  
 caaaaaacaa acaatcaaaa aaaaagacag tttattaaaa atgacacaaa 2800  
 tgactgggct aaatctactg tttcaaaaaa gtgtctttac aaaaaacaa 2850  
 aaaagaaaag aaatttattt attaaaaatt ctattgtgat ctaaagcaga 2900  
 caaaaa 2906

<210> 292

<211> 640

<212> PRT

<213> Homo Sapien

<400> 292

Met	Leu	Asn	Lys	Met	Thr	Leu	His	Pro	Gln	Gln	Ile	Met	Ile	Gly
1				5					10					15
Pro	Arg	Phe	Asn	Arg	Ala	Leu	Phe	Asp	Pro	Leu	Leu	Val	Val	Leu
			20						25					30
Leu	Ala	Leu	Gln	Leu	Leu	Val	Val	Ala	Gly	Leu	Val	Arg	Ala	Gln
			35						40					45
Thr	Cys	Pro	Ser	Val	Cys	Ser	Cys	Ser	Asn	Gln	Phe	Ser	Lys	Val
			50						55					60
Ile	Cys	Val	Arg	Lys	Asn	Leu	Arg	Glu	Val	Pro	Asp	Gly	Ile	Ser
			65						70					75
Thr	Asn	Thr	Arg	Leu	Leu	Asn	Leu	His	Glu	Asn	Gln	Ile	Gln	Ile
			80						85					90
Ile	Lys	Val	Asn	Ser	Phe	Lys	His	Leu	Arg	His	Leu	Glu	Ile	Leu
			95						100					105
Gln	Leu	Ser	Arg	Asn	His	Ile	Arg	Thr	Ile	Glu	Ile	Gly	Ala	Phe
			110						115					120
Asn	Gly	Leu	Ala	Asn	Leu	Asn	Thr	Leu	Glu	Leu	Phe	Asp	Asn	Arg
			125						130					135
Leu	Thr	Thr	Ile	Pro	Asn	Gly	Ala	Phe	Val	Tyr	Leu	Ser	Lys	Leu
			140						145					150
Lys	Glu	Leu	Trp	Leu	Arg	Asn	Asn	Pro	Ile	Glu	Ser	Ile	Pro	Ser

09909320-071801

				155					160					165
Tyr	Ala	Phe	Asn	Arg 170	Ile	Pro	Ser	Leu	Arg 175	Arg	Leu	Asp	Leu	Gly 180
Glu	Leu	Lys	Arg	Leu 185	Ser	Tyr	Ile	Ser	Glu 190	Gly	Ala	Phe	Glu	Gly 195
Leu	Ser	Asn	Leu	Arg 200	Tyr	Leu	Asn	Leu	Ala 205	Met	Cys	Asn	Leu	Arg 210
Glu	Ile	Pro	Asn	Leu 215	Thr	Pro	Leu	Ile	Lys 220	Leu	Asp	Glu	Leu	Asp 225
Leu	Ser	Gly	Asn	His 230	Leu	Ser	Ala	Ile	Arg 235	Pro	Gly	Ser	Phe	Gln 240
Gly	Leu	Met	His	Leu 245	Gln	Lys	Leu	Trp	Met 250	Ile	Gln	Ser	Gln	Ile 255
Gln	Val	Ile	Glu	Arg 260	Asn	Ala	Phe	Asp	Asn 265	Leu	Gln	Ser	Leu	Val 270
Glu	Ile	Asn	Leu	Ala 275	His	Asn	Asn	Leu	Thr 280	Leu	Leu	Pro	His	Asp 285
Leu	Phe	Thr	Pro	Leu 290	His	His	Leu	Glu	Arg 295	Ile	His	Leu	His	His 300
Asn	Pro	Trp	Asn	Cys 305	Asn	Cys	Asp	Ile	Leu 310	Trp	Leu	Ser	Trp	Trp 315
Ile	Lys	Asp	Met	Ala 320	Pro	Ser	Asn	Thr	Ala 325	Cys	Cys	Ala	Arg	Cys 330
Asn	Thr	Pro	Pro	Asn 335	Leu	Lys	Gly	Arg	Tyr 340	Ile	Gly	Glu	Leu	Asp 345
Gln	Asn	Tyr	Phe	Thr 350	Cys	Tyr	Ala	Pro	Val 355	Ile	Val	Glu	Pro	Pro 360
Ala	Asp	Leu	Asn	Val 365	Thr	Glu	Gly	Met	Ala 370	Ala	Glu	Leu	Lys	Cys 375
Arg	Ala	Ser	Thr	Ser 380	Leu	Thr	Ser	Val	Ser 385	Trp	Ile	Thr	Pro	Asn 390
Gly	Thr	Val	Met	Thr 395	His	Gly	Ala	Tyr	Lys 400	Val	Arg	Ile	Ala	Val 405
Leu	Ser	Asp	Gly	Thr 410	Leu	Asn	Phe	Thr	Asn 415	Val	Thr	Val	Gln	Asp 420

Thr Gly Met Tyr	Thr Cys Met Val Ser Asn Ser Val Gly Asn Thr	
	425	430 435
Thr Ala Ser Ala	Thr Leu Asn Val Thr Ala Ala Thr Thr Thr Pro	
	440	445 450
Phe Ser Tyr Phe	Ser Thr Val Thr Val Glu Thr Met Glu Pro Ser	
	455	460 465
Gln Asp Glu Ala	Arg Thr Thr Asp Asn Asn Val Gly Pro Thr Pro	
	470	475 480
Val Val Asp Trp	Glu Thr Thr Asn Val Thr Thr Ser Leu Thr Pro	
	485	490 495
Gln Ser Thr Arg	Ser Thr Glu Lys Thr Phe Thr Ile Pro Val Thr	
	500	505 510
Asp Ile Asn Ser	Gly Ile Pro Gly Ile Asp Glu Val Met Lys Thr	
	515	520 525
Thr Lys Ile Ile	Ile Gly Cys Phe Val Ala Ile Thr Leu Met Ala	
	530	535 540
Ala Val Met Leu	Val Ile Phe Tyr Lys Met Arg Lys Gln His His	
	545	550 555
Arg Gln Asn His	His Ala Pro Thr Arg Thr Val Glu Ile Ile Asn	
	560	565 570
Val Asp Asp Glu	Ile Thr Gly Asp Thr Pro Met Glu Ser His Leu	
	575	580 585
Pro Met Pro Ala	Ile Glu His Glu His Leu Asn His Tyr Asn Ser	
	590	595 600
Tyr Lys Ser Pro	Phe Asn His Thr Thr Thr Val Asn Thr Ile Asn	
	605	610 615
Ser Ile His Ser	Ser Val His Glu Pro Leu Leu Ile Arg Met Asn	
	620	625 630
Ser Lys Asp Asn	Val Gln Glu Thr Gln Ile	
	635	640

&lt;210&gt; 293

&lt;211&gt; 4053

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 293

agccgacgct gctcaagctg caactctggt gcagttggca gttcttttcg 50

09909320-071801

gtttccctcc tgctgtttgg gggcatgaaa gggcttcgcc gccgggagta 100  
 aaagaaggaa ttgaccgggc agcgcgaggg aggagcgcgc acgcgaccgc 150  
 gagggcgggc gtgcaccctc ggctggaagt ttgtgccggg ccccgagcgc 200  
 gcgccggctg ggagcttcgg gtagagacct aggcgcgtgg accgcgatga 250  
 gcgcgcgag cctccgtgcg cgcgccgcgg ggttggggct gctgctgtgc 300  
 gcggtgctgg ggcgcgtgg ccggtccgac agcggcggtc gcggggaact 350  
 cgggcagccc tctggggtag ccgccgagcg cccatgcccc actacctgcc 400  
 gctgcctcgg ggacctgctg gactgcagtc gtaagcggt agcgcgtctt 450  
 cccgagccac tcccgtcctg ggtcgtcgg ctggacttaa gtcacaacag 500  
 attatcttcc atcaaggcaa gttccatgag ccaccttcaa agccttcgag 550  
 aagtgaact gaacaacaat gaattggaga ccattccaaa tctgggacca 600  
 gtctcggcaa atattacact tctctccttg gctggaaaca ggattgttga 650  
 aatactcct gaacatctga aagagtttca gtcccttgaa actttggacc 700  
 ttagcagcaa caatatttca gagctccaaa ctgcatttcc agccctacag 750  
 ctcaaatacc tgtatctcaa cagcaaccga gtcacatcaa tggaacctgg 800  
 gtattttgac aatttgcca acacactcct tgtgttaaag ctgaacagga 850  
 accgaatctc agctatccca cccaagatgt ttaaactgcc ccaactgcaa 900  
 catctcgaat tgaaccgaaa caagattaaa aatgtagatg gactgacatt 950  
 ccaaggcctt ggtgctctga agtctctgaa aatgcaaaga aatggagtaa 1000  
 cgaaacttat ggatggagct ttttgggggc tgagcaacat ggaaattttg 1050  
 cagctggacc ataacaacct aacagagatt accaaaggct ggctttacgg 1100  
 cttgctgatg ctgcaggaaac ttcactctcag ccaaaatgcc atcaacagga 1150  
 tcagccctga tgccctgggag ttctgccaga agctcagtga gctggacct 1200  
 actttcaatc acttatcaag gttagatgat tcaagcttcc ttggcctaag 1250  
 cttactaaat aactgcaca ttgggaacaa cagagtcagc tacattgctg 1300  
 attgtgcctt ccgggggctt tccagtttaa agactttgga tctgaagaac 1350

09909320-071801

aatgaaatth cctggactat tgaagacatg aatggtgctt tctctgggct 1400  
 tgacaaactg aggcgactga tactccaagg aaatcggatc cgttctatta 1450  
 ctaaaaaagc cttcactggt ttggatgcat tggagcatct agacctgagt 1500  
 gacaacgcaa tcatgtcttt acaaggcaat gcattttcac aaatgaagaa 1550  
 actgcaacaa ttgcatttaa atacatcaag ctttttgtgc gattgccagc 1600  
 taaaatggct cccacagtgg gtggcgga aaactttca gagctttgta 1650  
 aatgccagtt gtgcccattc tcagctgcta aaaggaagaa gcatttttgc 1700  
 tgttagccca gatggctttg tgtgtgatga ttttcccaa cccagatca 1750  
 cggttcagcc agaaacacag tcggcaataa aaggttcaa tttgagtttc 1800  
 atctgctcag ctgccagcag cagtgattcc ccaatgactt ttgcttgga 1850  
 aaaagacaat gaactactgc atgatgctga aatggaaaat tatgcacacc 1900  
 tccgggocca aggtggcgag gtgatggagt ataccaccat ccttcggtg 1950  
 cgcgaggtgg aatttgccag tgaggggaaa tatcagtgtg tcatctcaa 2000  
 tcactttggt tcatctact ctgtcaaagc caagcttaca gtaaatatgc 2050  
 ttccctcatt caccaagacc cccatggatc tcaccatccg agctggggcc 2100  
 atggcacgct tggagtgtgc tgcgtgtggg caccagccc cccagatagc 2150  
 ctggcagaag gatgggggca cagacttccc agctgcacgg gagagacgca 2200  
 tgcattgtgat gcccaggat gacgtgttct ttatcgtgga tgtgaagata 2250  
 gaggacattg gggatatacag ctgcacagct cagaacagtg caggaagtat 2300  
 ttcagcaaat gcaactctga ctgtcctaga aacaccatca tttttgcggc 2350  
 cactgttgga ccgaactgta accaaggag aaacagccgt cctacagtgc 2400  
 attgctggag gaagccctcc ccctaaactg aactggacca aagatgatag 2450  
 cccattgggtg gtaaccgaga ggcacttttt tgcagcaggc aatcagcttc 2500  
 tgattattgt ggactcagat gtcagtgatg ctgggaaata cacatgtgag 2550  
 atgtctaaca cccttggcac tgagagagga aacgtgcgcc tcagtgtgat 2600  
 cccactcca acctgcgact cccctcagat gacagcccca tcgttagacg 2650  
 atgacggatg ggccactgtg ggtgtcgtga tcatagccgt ggtttgctgt 2700

gtggtgggca cgtcactcgt gtgggtgggc atcatatacc acacaaggcg 2750  
 gaggaatgaa gattgcagca ttaccaacac agatgagacc aacttgccag 2800  
 cagatattcc tagttatttg tcatctcagg gaacgttagc tgacaggcag 2850  
 gatgggtacg tgtcttcaga aagtggaaag caccaccagt ttgtcacatc 2900  
 ttcagggtgt ggatttttct taccacaaca tgacagtagt gggacctgcc 2950  
 atattgacaa tagcagtga gctgatgtgg aagctgccac agatctgttc 3000  
 ctttgtccgt ttttgggatc cacaggccct atgtatttga agggaaatgt 3050  
 gtatggctca gatccttttg aaacatatca tacaggttgc agtcctgacc 3100  
 caagaacagt tttaatggac cactatgagc ccagttacat aaagaaaaag 3150  
 gagtgtacc catgtttctca tccttcagaa gaatcctgcg aacggagctt 3200  
 cagtaatata tcgtggcctt cacatgtgag gaagctactt aacactagtt 3250  
 actctcacia tgaaggacct ggaatgaaaa atctgtgtct aaacaagtcc 3300  
 tcttttagatt ttagtgcaaa tccagagcca gcgtcggttg cctcgagtaa 3350  
 ttctttcatg ggtacctttg gaaaagctct caggagacct cacctagatg 3400  
 cctattcaag ctttggacag ccatcagatt gtcagccaag agccttttat 3450  
 ttgaaagctc attcttcccc agacttggac tctgggtcag aggaagatgg 3500  
 gaaagaaagg acagattttc aggaagaaaa tcacatttgt acctttaaac 3550  
 agactttaga aaactacagg actccaaatt ttcagtctta tgacttggac 3600  
 acatagactg aatgagacca aaggaaaagc ttaacatact acctcaagtg 3650  
 aacttttatt taaaagagag agaactctat gttttttaaa tggagttatg 3700  
 aattttaaaa ggataaaaaat gctttattta tacagatgaa ccaaaattac 3750  
 aaaaagttat gaaaattttt atactgggaa tgatgctcat ataagaatac 3800  
 ctttttaaac tatttttttaa ctttgtttta tgcaaaaaag tatcttacgt 3850  
 aaattaatga tataaatcat gattatttta tgtattttta taatgccaga 3900  
 tttcttttta tggaaaatga gttactaaag catttttaaat aatacctgcc 3950  
 ttgtaccatt ttttaaatag aagttacttc attatatattt gcacattata 4000

tttaataaaaa tgtgtcaatt tgaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4050

aaa 4053

<210> 294

<211> 1119

<212> PRT

<213> Homo Sapien

<400> 294

Met Ser Ala Pro Ser Leu Arg Ala Arg Ala Ala Gly Leu Gly Leu  
1 5 10 15

Leu Leu Cys Ala Val Leu Gly Arg Ala Gly Arg Ser Asp Ser Gly  
20 25 30

Gly Arg Gly Glu Leu Gly Gln Pro Ser Gly Val Ala Ala Glu Arg  
35 40 45

Pro Cys Pro Thr Thr Cys Arg Cys Leu Gly Asp Leu Leu Asp Cys  
50 55 60

Ser Arg Lys Arg Leu Ala Arg Leu Pro Glu Pro Leu Pro Ser Trp  
65 70 75

Val Ala Arg Leu Asp Leu Ser His Asn Arg Leu Ser Phe Ile Lys  
80 85 90

Ala Ser Ser Met Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu  
95 100 105

Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser  
110 115 120

Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu  
125 130 135

Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu  
140 145 150

Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro  
155 160 165

Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr  
170 175 180

Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu  
185 190 195

Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys  
200 205 210

Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn

09909320-071801



				215					220					225
Lys	Ile	Lys	Asn	Val	Asp	Gly	Leu	Thr	Phe	Gln	Gly	Leu	Gly	Ala
				230					235					240
Leu	Lys	Ser	Leu	Lys	Met	Gln	Arg	Asn	Gly	Val	Thr	Lys	Leu	Met
				245					250					255
Asp	Gly	Ala	Phe	Trp	Gly	Leu	Ser	Asn	Met	Glu	Ile	Leu	Gln	Leu
				260					265					270
Asp	His	Asn	Asn	Leu	Thr	Glu	Ile	Thr	Lys	Gly	Trp	Leu	Tyr	Gly
				275					280					285
Leu	Leu	Met	Leu	Gln	Glu	Leu	His	Leu	Ser	Gln	Asn	Ala	Ile	Asn
				290					295					300
Arg	Ile	Ser	Pro	Asp	Ala	Trp	Glu	Phe	Cys	Gln	Lys	Leu	Ser	Glu
				305					310					315
Leu	Asp	Leu	Thr	Phe	Asn	His	Leu	Ser	Arg	Leu	Asp	Asp	Ser	Ser
				320					325					330
Phe	Leu	Gly	Leu	Ser	Leu	Leu	Asn	Thr	Leu	His	Ile	Gly	Asn	Asn
				335					340					345
Arg	Val	Ser	Tyr	Ile	Ala	Asp	Cys	Ala	Phe	Arg	Gly	Leu	Ser	Ser
				350					355					360
Leu	Lys	Thr	Leu	Asp	Leu	Lys	Asn	Asn	Glu	Ile	Ser	Trp	Thr	Ile
				365					370					375
Glu	Asp	Met	Asn	Gly	Ala	Phe	Ser	Gly	Leu	Asp	Lys	Leu	Arg	Arg
				380					385					390
Leu	Ile	Leu	Gln	Gly	Asn	Arg	Ile	Arg	Ser	Ile	Thr	Lys	Lys	Ala
				395					400					405
Phe	Thr	Gly	Leu	Asp	Ala	Leu	Glu	His	Leu	Asp	Leu	Ser	Asp	Asn
				410					415					420
Ala	Ile	Met	Ser	Leu	Gln	Gly	Asn	Ala	Phe	Ser	Gln	Met	Lys	Lys
				425					430					435
Leu	Gln	Gln	Leu	His	Leu	Asn	Thr	Ser	Ser	Leu	Leu	Cys	Asp	Cys
				440					445					450
Gln	Leu	Lys	Trp	Leu	Pro	Gln	Trp	Val	Ala	Glu	Asn	Asn	Phe	Gln
				455					460					465
Ser	Phe	Val	Asn	Ala	Ser	Cys	Ala	His	Pro	Gln	Leu	Leu	Lys	Gly
				470					475					480

109509320.071301

Arg Ser Ile Phe	Ala Val Ser Pro Asp	Gly Phe Val Cys Asp Asp
485		490 495
Phe Pro Lys Pro	Gln Ile Thr Val Gln	Pro Glu Thr Gln Ser Ala
500		505 510
Ile Lys Gly Ser	Asn Leu Ser Phe Ile	Cys Ser Ala Ala Ser Ser
515		520 525
Ser Asp Ser Pro	Met Thr Phe Ala Trp	Lys Lys Asp Asn Glu Leu
530		535 540
Leu His Asp Ala	Glu Met Glu Asn Tyr	Ala His Leu Arg Ala Gln
545		550 555
Gly Gly Glu Val	Met Glu Tyr Thr Thr	Ile Leu Arg Leu Arg Glu
560		565 570
Val Glu Phe Ala	Ser Glu Gly Lys Tyr	Gln Cys Val Ile Ser Asn
575		580 585
His Phe Gly Ser	Ser Tyr Ser Val Lys	Ala Lys Leu Thr Val Asn
590		595 600
Met Leu Pro Ser	Phe Thr Lys Thr Pro	Met Asp Leu Thr Ile Arg
605		610 615
Ala Gly Ala Met	Ala Arg Leu Glu Cys	Ala Ala Val Gly His Pro
620		625 630
Ala Pro Gln Ile	Ala Trp Gln Lys Asp	Gly Gly Thr Asp Phe Pro
635		640 645
Ala Ala Arg Glu	Arg Arg Met His Val	Met Pro Glu Asp Asp Val
650		655 660
Phe Phe Ile Val	Asp Val Lys Ile Glu	Asp Ile Gly Val Tyr Ser
665		670 675
Cys Thr Ala Gln	Asn Ser Ala Gly Ser	Ile Ser Ala Asn Ala Thr
680		685 690
Leu Thr Val Leu	Glu Thr Pro Ser Phe	Leu Arg Pro Leu Leu Asp
695		700 705
Arg Thr Val Thr	Lys Gly Glu Thr Ala	Val Leu Gln Cys Ile Ala
710		715 720
Gly Gly Ser Pro	Pro Pro Lys Leu Asn	Trp Thr Lys Asp Asp Ser
725		730 735
Pro Leu Val Val	Thr Glu Arg His Phe	Phe Ala Ala Gly Asn Gln
740		745 750

FOR 071801 02E60660

Leu	Leu	Ile	Ile	Val	Asp	Ser	Asp	Val	Ser	Asp	Ala	Gly	Lys	Tyr	755	760	765
Thr	Cys	Glu	Met	Ser	Asn	Thr	Leu	Gly	Thr	Glu	Arg	Gly	Asn	Val	770	775	780
Arg	Leu	Ser	Val	Ile	Pro	Thr	Pro	Thr	Cys	Asp	Ser	Pro	Gln	Met	785	790	795
Thr	Ala	Pro	Ser	Leu	Asp	Asp	Asp	Gly	Trp	Ala	Thr	Val	Gly	Val	800	805	810
Val	Ile	Ile	Ala	Val	Val	Cys	Cys	Val	Val	Gly	Thr	Ser	Leu	Val	815	820	825
Trp	Val	Val	Ile	Ile	Tyr	His	Thr	Arg	Arg	Arg	Asn	Glu	Asp	Cys	830	835	840
Ser	Ile	Thr	Asn	Thr	Asp	Glu	Thr	Asn	Leu	Pro	Ala	Asp	Ile	Pro	845	850	855
Ser	Tyr	Leu	Ser	Ser	Gln	Gly	Thr	Leu	Ala	Asp	Arg	Gln	Asp	Gly	860	865	870
Tyr	Val	Ser	Ser	Glu	Ser	Gly	Ser	His	His	Gln	Phe	Val	Thr	Ser	875	880	885
Ser	Gly	Ala	Gly	Phe	Phe	Leu	Pro	Gln	His	Asp	Ser	Ser	Gly	Thr	890	895	900
Cys	His	Ile	Asp	Asn	Ser	Ser	Glu	Ala	Asp	Val	Glu	Ala	Ala	Thr	905	910	915
Asp	Leu	Phe	Leu	Cys	Pro	Phe	Leu	Gly	Ser	Thr	Gly	Pro	Met	Tyr	920	925	930
Leu	Lys	Gly	Asn	Val	Tyr	Gly	Ser	Asp	Pro	Phe	Glu	Thr	Tyr	His	935	940	945
Thr	Gly	Cys	Ser	Pro	Asp	Pro	Arg	Thr	Val	Leu	Met	Asp	His	Tyr	950	955	960
Glu	Pro	Ser	Tyr	Ile	Lys	Lys	Lys	Glu	Cys	Tyr	Pro	Cys	Ser	His	965	970	975
Pro	Ser	Glu	Glu	Ser	Cys	Glu	Arg	Ser	Phe	Ser	Asn	Ile	Ser	Trp	980	985	990
Pro	Ser	His	Val	Arg	Lys	Leu	Leu	Asn	Thr	Ser	Tyr	Ser	His	Asn	995	1000	1005
Glu	Gly	Pro	Gly	Met	Lys	Asn	Leu	Cys	Leu	Asn	Lys	Ser	Ser	Leu			

FOI b7D b7E b7F

1010	1015	1020
Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn		
1025	1030	1035
Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu		
1040	1045	1050
Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg		
1055	1060	1065
Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly		
1070	1075	1080
Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn		
1085	1090	1095
His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro		
1100	1105	1110
Asn Phe Gln Ser Tyr Asp Leu Asp Thr		
1115		

&lt;210&gt; 295

&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 295

ggaaccgaat ctcagcta 18

&lt;210&gt; 296

&lt;211&gt; 19

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 296

cctaaactga actggacca 19

&lt;210&gt; 297

&lt;211&gt; 19

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

FOR "0" FILE 60660

<400> 297  
ggctggagac actgaacct 19

<210> 298  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 298  
acagctgcac agctcagaac agtg 24

<210> 299

<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 299  
cattcccagt ataaaaattt tc 22

<210> 300  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 300  
gggtcttggt gaatgagg 18

<210> 301  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 301  
gtgcctctcg gttaccacca atgg 24

<210> 302  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 302

gcggccactg ttggaccgaa ctgtaaccaa gggagaaaca gccgtcctac 50

<210> 303

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 303

gcctttgaca accttcagtc actagtgg 28

<210> 304

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 304

cccatgtgt ccatgactgt tccc 24

<210> 305

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 305

tactgcctca tgacctcttc actcccttgc atcatcttag agcgg 45

<210> 306

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 306

actccaagga aatcgatcc gttc 24

<210> 307

<211> 24

09009320.01301

<212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 307  
 ttagcagctg aggatgggca caac 24

<210> 308  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 308  
 actccaagga aatcgatcc gttc 24

<210> 309  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 309  
 gccttcactg gtttggatgc attggagcat ctagacctga gtgacaacgc 50

<210> 310  
 <211> 3296  
 <212> DNA  
 <213> Homo Sapien

<400> 310  
 caaaacttgc gtcgcgagaga gcgcccagct tgacttgaat ggaaggagcc 50  
 cgagcccgcg gagcgagct gagactgggg gagcgcgctc gccctgtggg 100  
 gcgcccgtcg gcgcccgggg gcagcaggga aggggaagct gtggtctgcc 150  
 ctgctccacg aggcgccact ggtgtgaacc gggagagccc ctgggtgggc 200  
 ccgtccccta tccctccttt atatagaaac cttccacact gggaaggcag 250  
 cggcgaggca ggagggtca tggtgagcaa ggaggccggc tgatctgcag 300  
 gcgcacagca ttccgagttt acagattttt acagatacca aatggaaggc 350  
 gaggaggcag aacagcctgc ctggttccat cagccctggc gcccaggcgc 400

atctgactcg gcacccccctg caggcaccat ggcccagagc cgggtgctgc 450  
 tgctcctgct gctgctgccg ccacagctgc acctgggacc tgtgcttgcc 500  
 gtgagggccc caggatttgg ccgaagtggc ggccacagcc tgagccccga 550  
 agagaacgaa tttgcggagg aggagccggt gctggtactg agccctgagg 600  
 agcccgggcc tggcccagcc gcggtcagct gcccccgaga ctgtgectgt 650  
 tcccaggagg gcgtcgtgga ctgtggcggt attgacctgc gtgagttccc 700  
 gggggacctg cctgagcaca ccaaccacct atctctgcag aacaaccagc 750  
 tggaaaagat ctacctgag gagctctccc ggctgcaccg gctggagaca 800  
 ctgaacctgc aaaacaaccg cctgacttcc cgagggctcc cagagaaggc 850  
 gtttgagcat ctgaccaacc tcaattacct gtacttggcc aataacaagc 900  
 tgaccttggc accccgcttc ctgccaaacg ccctgatcag tgtggacttt 950  
 gctgccaaact atctcaccia gatctatggg ctcacctttg gccagaagcc 1000  
 aaacttgagg tctgtgtacc tgcacaacaa caagctggca gacgccgggc 1050  
 tgccggacaa catgttcaac ggctccagca acgtcgaggt cctcatcctg 1100  
 tccagcaact tctgcgcca cgtgcccag cacctgccgc ctgccctgta 1150  
 caagctgcac ctcaagaaca acaagctgga gaagatcccc ccgggggcct 1200  
 tcagcgagct gagcagcctg cgcgagctat acctgcagaa caactacctg 1250  
 actgacgagg gectggacaa cgagaccttc tggaagctct ccagcctgga 1300  
 gtacctggat ctgtccagca acaacctgtc tcgggtccca gctgggctgc 1350  
 cgcgcagcct ggtgctgctg cacttggaga agaacgccat ccggagcgtg 1400  
 gacgcgaatg tgctgacccc catccgcagc ctggagtacc tgctgctgca 1450  
 cagcaaccag ctgcgggagc agggcatcca cccactggcc ttccagggcc 1500  
 tcaagcgggt gcacacgggtg cacctgtaca acaacgcgct ggagcgcgtg 1550  
 cccagtggcc tgctcgccg cgtgcgcacc ctcatgatcc tgcacaacca 1600  
 gatcacaggc attggccgcg aagactttgc caccacctac ttctggagg 1650  
 agtcaacct cagctacaac cgcatacca gccacaggt gcaccgcgac 1700



gccttccgca agctgcgcct gctgcgctcg ctggacctgt cgggcaaccg 1750  
 gctgcacacg ctgccacctg ggctgcctcg aaatgtccat gtgctgaagg 1800  
 tcaagcgcaa tgagctggct gccttggcac gaggggcgct ggcgggcatg 1850  
 gctcagctgc gtgagctgta cctcaccagc aaccgactgc gcagccgagc 1900  
 cctggggccc cgtgcctggg tggacctgcg ccatctgcag ctgctggaca 1950  
 tcgcccggaa tcagctcaca gagatccccg aggggctccc cgagtcactt 2000  
 gagtacctgt acctgcagaa caacaagatt agtgcggtgc ccgccaatgc 2050  
 cttcgactcc acgcccgaacc tcaaggggat ctttctcagg tttacaagc 2100  
 tggtgtggg ctccgtggtg gacagtgcct tccggaggct gaagcacctg 2150  
 caggtcttgg acattgaagg caacttagag tttggtgaca tttccaagga 2200  
 ccgtggccgc ttggggaagg aaaaggagga ggaggaagag gaggaggagg 2250  
 aggaagagga aacaagatag tgacaagggt atgcagatgt gacctaggat 2300  
 gatggaccgc cggactcttt tctgcagcac acgcctgtgt gctgtgagcc 2350  
 cccactctg ccgtgctcac acagacacac ccagctgcac acatgaggca 2400  
 tcccacatga cacgggctga cacagtctca tatccccacc ccttcccacg 2450  
 gcgtgtccca cggccagaca catgcacaca catcacacc tcaaacacc 2500  
 agctcagcca cacacaacta cctccaaac caccacagtc tctgtcacac 2550  
 cccactacc gctgccacgc cctctgaatc atgcaggga gggctctgcc 2600  
 ctgcctggc acacacaggc acccattccc tccccctgct gacatgtgta 2650  
 tgcgtatgca tacacaccac acacacacac atgcacaagt catgtgcgaa 2700  
 cagccctcca aagcctatgc cacagacagc tcttgcacca gccagaatca 2750  
 gccatagcag ctgcgcgtct gccctgtcca tctgtccgtc cgttccctgg 2800  
 agaagacaca agggatatca tgctctgtgg ccaggtgcct gccaccctct 2850  
 ggaactcaca aaagctggct ttatttcctt tcccatccta tggggacagg 2900  
 agccttcagg actgctggcc tggcctggcc caccctgctc ctccagggtgc 2950  
 tgggcagtca ctctgctaag agtccctccc tgccacgccc tggcaggaca 3000  
 caggcacttt tccaatgggc aagcccagtg gaggcaggat gggagagccc 3050

cctgggtgct gctggggcct tggggcagga gtgaagcaga ggtgatgggg 3100  
 ctgggctgag ccagggagga aggaccacgc tgcacctagg agacaccttt 3150  
 gttcttcagg cctgtggggg aagttccggg tgcctttatt ttttattctt 3200  
 ttctaaggaa aaaaatgata aaaatctcaa agctgatttt tcttggtata 3250  
 gaaaaactaa tataaaagca ttatccctat ccctgcaaaa aaaaaa 3296

<210> 311

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 311

gcattggcgcg cgagactttg cc 22

<210> 312

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 312

gcggccacgcg tccttggaat tg 22

<210> 313

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 313

tggaggagct caacctcagc tacaaccgca tcaccagccc acagg 45

<210> 314

<211> 3003

<212> DNA

<213> Homo Sapien

<400> 314

gggaggggggc tccggggcgc ggcagcagca cctgctccgg ccgcgcgcc 50

cgccgctgtc ctccgggagc ggcagcagta gcccgggcgg cgagggctgg 100

FOET 20" 02E60660

gggttcctcg agactctcag aggggcgcct cccatcggcg cccaccaccc 150  
 caacctgttc ctgcgcgcgc actgcgctgc gccccaggac ccgctgcccc 200  
 acatggattt tctcctggcg ctggtgctgg tatectcgct ctacctgcag 250  
 gcggccgcgc agttcgacgg gaggtggccc aggcaaatag tgtcatcgat 300  
 tggcctatgt cgttatggtg ggaggattga ctgctgctgg ggctgggctc 350  
 gccagtcttg gggacagtgt cagcctgtgt gccaaaccag atgcaaacat 400  
 ggtgaatgta tcggggccaaa caagtgcag tgtcatcctg gttatgctgg 450  
 aaaaacctgt aatcaagatc taaatgagtg tggcctgaag ccccggcct 500  
 gtaagcacag gtgcatgaac acttacggca gctacaagtg ctactgtctc 550  
 aacggatata tgctcatgcc ggatgggttc tgctcaagtg ccctgacctg 600  
 ctccatggca aactgtcagt atggctgtga tgttggttaa ggacaaatac 650  
 ggtgccagtg cccatccctt ggctgcacc tggctcctga tgggaggacc 700  
 tgtgtagatg ttgatgaatg tgctacagga agagcctcct gccctagatt 750  
 taggcaatgt gtcaacactt ttgggagcta catctgcaag tgtcataaag 800  
 gcttcgatct catgtatatt ggaggcaa atcaatgtca tgacatagac 850  
 gaatgctcac ttggtcagta tcagtgcagc agctttgctc gatgttataa 900  
 cgtacgtggg tctacaagt gcaaagttaa agaaggatac caggggtgatg 950  
 gactgacttg tgtgtatata ccaaaagtta tgattgaacc ttcaggcca 1000  
 attcatgtac caaagggaat tggtagcatt ttaaagggtg acacaggaaa 1050  
 taataattgg attcctgatg ttggaagtac ttggtggcct ccgaagacac 1100  
 catatattcc tctatcatt accaacaggc ctacttctaa gccacaaca 1150  
 agacctacac caaagccaac accaattcct actccaccac caccaccacc 1200  
 cctgccaca gagctcagaa cacctctacc acctacaacc ccagaaaggc 1250  
 caaccaccgg actgacaact atagcaccag ctgccagtac acctccagga 1300  
 gggattacag ttgacaacag ggtacagaca gacctcaga aaccagagg 1350  
 agatgtgttc agtgttctgg tacacagttg taattttgac catggacttt 1400

gtggatggat cagggagaaa gacaatgact tgcactggga accaatcagg 1450  
 gaccagcag gtggacaata tctgacagtg tcggcagcca aagccccagg 1500  
 gggaaaagct gcacgcttgg tgctacctct cggccgcctc atgcattcag 1550  
 gggacctgtg cctgtcattc aggcacaagg tgacgggggt gcactctggc 1600  
 acactccagg tgtttgtgag aaaacacggt gccacaggag cagccctgtg 1650  
 gggaagaaat ggtggccatg gctggaggca aacacagatc accttgcgag 1700  
 gggctgacat caagagcgaa tcacaaagat gattaaagg ttggaaaaaa 1750  
 agatctatga tggaaaatta aaggaactgg gattattgag cctggagaag 1800  
 agaagactga ggggcaaacc attgatgggt ttcaagtata tgaagggttg 1850  
 gcacagagag ggtggcgacc agctgttctc catatgcact aagaatagaa 1900  
 caagaggaaa ctggcttaga ctagagtata agggagcatt tcttggcagg 1950  
 ggccattgtt agaatacttc ataaaaaag aagtgtgaaa atctcagtat 2000  
 ctctctctct ttctaaaaaa ttagataaaa atttgtctat ttaagatggg 2050  
 taaagatggt cttacccaag gaaaagtaac aaattataga atttcccaa 2100  
 agatgttttg atcctactag tagtatgcag tgaaaatctt tagaactaaa 2150  
 taatttggac aaggcttaat ttaggcattt ccctcttgac ctctaatgg 2200  
 agagggattg aaaggggaag agcccaccaa atgctgagct cactgaaata 2250  
 tctctccctt atggcaatcc tagcagtatt aaagaaaaaa ggaaactatt 2300  
 tattccaaat gagagtatga tggacagata ttttagtatc tcagtaatgt 2350  
 cctagtgtgg cggtggtttt caatgtttct tcatggtaaa ggtataagcc 2400  
 tttcatttgt tcaatggatg atgtttcaga tttttttttt ttttaagagat 2450  
 cttcaagga acacagttca gagagatttt catcgggtgc attctctctg 2500  
 cttcgtgtgt gacaagttat cttggctgct gagaaagagt gccctgcccc 2550  
 acaccggcag acctttcctt cacctcatca gtatgattca gtttctctta 2600  
 tcaattggac tctcccagg tccacagaac agtaatat tttgaacaat 2650  
 aggtacaata gaaggtcttc tgtcatttaa cctggtaaag gcagggctgg 2700  
 agggggaaaa taaatcatta agcctttgag taacggcaga atatatggct 2750

gtagatccat ttttaatggt tcatttcctt tatggtcata taactgcaca 2800  
 gctgaagatg aaaggggaaa ataaatgaaa attttacttt tcgatgccaa 2850  
 tgatacattg cactaaactg atggaagaag ttatccaaag tactgtataa 2900  
 catcttggtt attatttaat gttttctaaa ataaaaaatg ttagtggttt 2950  
 tccaaattggc ctaataaaaa caattatttg taaataaaaa cactgttagt 3000  
 at 3003

<210> 315  
 <211> 509  
 <212> PRT  
 <213> Homo Sapien

<400> 315  
 Met Asp Phe Leu Leu Ala Leu Val Leu Val Ser Ser Leu Tyr Leu  
     1                    5                    10                    15  
 Gln Ala Ala Ala Glu Phe Asp Gly Arg Trp Pro Arg Gln Ile Val  
                     20                    25                    30  
 Ser Ser Ile Gly Leu Cys Arg Tyr Gly Gly Arg Ile Asp Cys Cys  
                     35                    40                    45  
 Trp Gly Trp Ala Arg Gln Ser Trp Gly Gln Cys Gln Pro Val Cys  
                     50                    55                    60  
 Gln Pro Arg Cys Lys His Gly Glu Cys Ile Gly Pro Asn Lys Cys  
                     65                    70                    75  
 Lys Cys His Pro Gly Tyr Ala Gly Lys Thr Cys Asn Gln Asp Leu  
                     80                    85                    90  
 Asn Glu Cys Gly Leu Lys Pro Arg Pro Cys Lys His Arg Cys Met  
                     95                    100                    105  
 Asn Thr Tyr Gly Ser Tyr Lys Cys Tyr Cys Leu Asn Gly Tyr Met  
                     110                    115                    120  
 Leu Met Pro Asp Gly Ser Cys Ser Ser Ala Leu Thr Cys Ser Met  
                     125                    130                    135  
 Ala Asn Cys Gln Tyr Gly Cys Asp Val Val Lys Gly Gln Ile Arg  
                     140                    145                    150  
 Cys Gln Cys Pro Ser Pro Gly Leu His Leu Ala Pro Asp Gly Arg  
                     155                    160                    165

09909320-071801

Thr Cys Val Asp	Val Asp Glu Cys Ala	Thr Gly Arg Ala Ser Cys
170	175	180
Pro Arg Phe Arg	Gln Cys Val Asn Thr	Phe Gly Ser Tyr Ile Cys
185	190	195
Lys Cys His Lys	Gly Phe Asp Leu Met	Tyr Ile Gly Gly Lys Tyr
200	205	210
Gln Cys His Asp	Ile Asp Glu Cys Ser	Leu Gly Gln Tyr Gln Cys
215	220	225
Ser Ser Phe Ala	Arg Cys Tyr Asn Val	Arg Gly Ser Tyr Lys Cys
230	235	240
Lys Cys Lys Glu	Gly Tyr Gln Gly Asp	Gly Leu Thr Cys Val Tyr
245	250	255
Ile Pro Lys Val	Met Ile Glu Pro Ser	Gly Pro Ile His Val Pro
260	265	270
Lys Gly Asn Gly	Thr Ile Leu Lys Gly	Asp Thr Gly Asn Asn Asn
275	280	285
Trp Ile Pro Asp	Val Gly Ser Thr Trp	Trp Pro Pro Lys Thr Pro
290	295	300
Tyr Ile Pro Pro	Ile Ile Thr Asn Arg	Pro Thr Ser Lys Pro Thr
305	310	315
Thr Arg Pro Thr	Pro Lys Pro Thr Pro	Ile Pro Thr Pro Pro Pro
320	325	330
Pro Pro Pro Leu	Pro Thr Glu Leu Arg	Thr Pro Leu Pro Pro Thr
335	340	345
Thr Pro Glu Arg	Pro Thr Thr Gly Leu	Thr Thr Ile Ala Pro Ala
350	355	360
Ala Ser Thr Pro	Pro Gly Gly Ile Thr	Val Asp Asn Arg Val Gln
365	370	375
Thr Asp Pro Gln	Lys Pro Arg Gly Asp	Val Phe Ser Val Leu Val
380	385	390
His Ser Cys Asn	Phe Asp His Gly Leu	Cys Gly Trp Ile Arg Glu
395	400	405
Lys Asp Asn Asp	Leu His Trp Glu Pro	Ile Arg Asp Pro Ala Gly
410	415	420
Gly Gln Tyr Leu	Thr Val Ser Ala Ala	Lys Ala Pro Gly Gly Lys

FOR "0" 02E60660

425	430	435
Ala Ala Arg Leu Val Leu Pro Leu Gly Arg Leu Met His Ser Gly		
440	445	450
Asp Leu Cys Leu Ser Phe Arg His Lys Val Thr Gly Leu His Ser		
455	460	465
Gly Thr Leu Gln Val Phe Val Arg Lys His Gly Ala His Gly Ala		
470	475	480
Ala Leu Trp Gly Arg Asn Gly Gly His Gly Trp Arg Gln Thr Gln		
485	490	495
Ile Thr Leu Arg Gly Ala Asp Ile Lys Ser Glu Ser Gln Arg		
500	505	

&lt;210&gt; 316

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 316

gatggttcct gctcaagtgc cctg 24

&lt;210&gt; 317

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 317

ttgcacttgt aggacccacg tacg 24

&lt;210&gt; 318

&lt;211&gt; 50

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 318

ctgatgggag gacctgtgta gatgttgatg aatgtgctac aggaagagcc 50

&lt;210&gt; 319

&lt;211&gt; 2110

&lt;212&gt; DNA

T03T20"02E60660

<213> Homo Sapien

<400> 319

```

cttctttgaa aaggattatc acctgatcag gttctctctg catttgcccc 50
tttagattgt gaaatgtggc tcaaggtctt cacaactttc ctttcctttg 100
caacaggtgc ttgctcgggg ctgaaggtga cagtgccatc acacactgtc 150
catggcgctc gaggtcaggc cctctacctc cccgtccact atggcttcca 200
cactccagca tcagacatcc agatcatatg gctatttgag agaccccaca 250
caatgccccaa atacttactg ggctctgtga ataagtctgt ggttcctgac 300
ttggaatacc aacacaagtt caccatgatg ccaccaatg catctctgct 350
tatcaacca ctgcagttcc ctgatgaagg caattacatc gtgaaggtca 400
acattcaggg aaatggaact ctatctgccg gtcagaagat acaagtcacg 450
gttgatgatc ctgtcacaaa gccagtggtg cagattcatc ctccctctgg 500
ggctgtggag tatgtgggga acatgacctc gacatgccat gtggaagggg 550
gcactcggct agcttaccaa tggctaaaaa atgggagacc tgtccacacc 600
agctccacct actccttttc tccccaaaac aatacccttc atattgctcc 650
agtaaccaag gaagacattg ggaattacag ctgcctgggtg aggaaccctg 700
tcagtgaat ggaaagtgat atcattatgc ccatcatata ttatggacct 750
tatggacttc aagtgaattc tgataaaggg ctaaaagtag ggggaagtgtt 800
tactgttgac cttggagagg ccatcctatt tgattgttct gctgattctc 850
atccccccaa cacctactcc tggattagga ggactgacaa tactacatat 900
atcattaagc atgggcctcg cttagaagtt gcatctgaga aagtagccca 950
gaagacaatg gactatgtgt gctgtgctta caacaacata accggcaggc 1000
aagatgaaac tcatttcaca gttatcatca cttccgtagg actggagaag 1050
cttgcacaga aaggaaaatc attgtcacct ttagcaagta taactggaat 1100
atcactatct ttgattatat ccatgtgtct tctcttctc tggaaaaaat 1150
atcaacccta caaagttata aaacagaaac tagaaggcag gccagaaaca 1200
gaatacagga aagctcaaac attttcaggc catgaagatg ctctggatga 1250

```

09909320.07.1804



ctctggaata tatgaatttg ttgcttttcc agatgtttct ggtgtttcca 1300  
 ggattccaag caggtctggt ccagcctctg attgtgtatc ggggcaagat 1350  
 ttgcacagta cagtgtatga agttattcag cacatccctg cccagcagca 1400  
 agaccatcca gagtgaactt tcatgggcta aacagtacat tcgagtgaaa 1450  
 ttctgaagaa acattttaag gaaaaacagt ggaaaagtat attaactctgg 1500  
 aatcagtga gaaaccagga ccaacacctc ttactcatta ttcctttaca 1550  
 tgcagaatag aggcatttat gcaaattgaa ctgcagggtt ttcagcatat 1600  
 acacaatgtc ttgtgcaaca gaaaaacatg ttgggggaaat attcctcagt 1650  
 ggagagtcgt tctcatgctg acggggagaa cgaaagtgc aggggtttcc 1700  
 tcataagttt tgtatgaaat atctctacaa acctcaatta gttctactct 1750  
 acactttcac tatcatcaac actgagacta tctgtctca cctacaaatg 1800  
 tggaaacttt acattgttcg atttttcagc agactttgtt ttattaaatt 1850  
 tttattagt ttaagaatgc taaatttatg tttcaatttt atttccaaat 1900  
 ttctatcttg ttatttgtac aacaaagtaa taaggatggg tgtcacaaaa 1950  
 aaaaaactat gccttctctt ttttttcaat caccagtagt atttttgaga 2000  
 agacttgtga acacttaagg aatgactat taaagtctta tttttatatt 2050  
 tttcaaggaa agatggattc aaataaatta ttctgttttt gcttttaaaa 2100  
 aaaaaaaaaa 2110

<210> 320

<211> 450

<212> PRT

<213> Homo Sapien

<400> 320

Met	Trp	Leu	Lys	Val	Phe	Thr	Thr	Phe	Leu	Ser	Phe	Ala	Thr	Gly
1				5					10					15

Ala	Cys	Ser	Gly	Leu	Lys	Val	Thr	Val	Pro	Ser	His	Thr	Val	His
				20					25					30

Gly	Val	Arg	Gly	Gln	Ala	Leu	Tyr	Leu	Pro	Val	His	Tyr	Gly	Phe
				35					40					45

His	Thr	Pro	Ala	Ser	Asp	Ile	Gln	Ile	Ile	Trp	Leu	Phe	Glu	Arg
				50					55					60

FOR "02E60660"

Pro His Thr Met	Pro Lys Tyr Leu Leu Gly	Ser Val Asn Lys Ser
65	70	75
Val Val Pro Asp	Leu Glu Tyr Gln His Lys Phe Thr Met Met Pro	
80	85	90
Pro Asn Ala Ser	Leu Leu Ile Asn Pro Leu Gln Phe Pro Asp Glu	
95	100	105
Gly Asn Tyr Ile	Val Lys Val Asn Ile Gln Gly Asn Gly Thr Leu	
110	115	120
Ser Ala Ser Gln	Lys Ile Gln Val Thr Val Asp Asp Pro Val Thr	
125	130	135
Lys Pro Val Val	Gln Ile His Pro Pro Ser Gly Ala Val Glu Tyr	
140	145	150
Val Gly Asn Met	Thr Leu Thr Cys His Val Glu Gly Gly Thr Arg	
155	160	165
Leu Ala Tyr Gln	Trp Leu Lys Asn Gly Arg Pro Val His Thr Ser	
170	175	180
Ser Thr Tyr Ser	Phe Ser Pro Gln Asn Asn Thr Leu His Ile Ala	
185	190	195
Pro Val Thr Lys	Glu Asp Ile Gly Asn Tyr Ser Cys Leu Val Arg	
200	205	210
Asn Pro Val Ser	Glu Met Glu Ser Asp Ile Ile Met Pro Ile Ile	
215	220	225
Tyr Tyr Gly Pro	Tyr Gly Leu Gln Val Asn Ser Asp Lys Gly Leu	
230	235	240
Lys Val Gly Glu	Val Phe Thr Val Asp Leu Gly Glu Ala Ile Leu	
245	250	255
Phe Asp Cys Ser	Ala Asp Ser His Pro Pro Asn Thr Tyr Ser Trp	
260	265	270
Ile Arg Arg Thr	Asp Asn Thr Thr Tyr Ile Ile Lys His Gly Pro	
275	280	285
Arg Leu Glu Val	Ala Ser Glu Lys Val Ala Gln Lys Thr Met Asp	
290	295	300
Tyr Val Cys Cys	Ala Tyr Asn Asn Ile Thr Gly Arg Gln Asp Glu	
305	310	315
Thr His Phe Thr	Val Ile Ile Thr Ser Val Gly Leu Glu Lys Leu	

FOI b7D b7E b7F

	320		325		330
Ala Gln Lys Gly	Lys Ser Leu Ser Pro	Leu Ala Ser Ile Thr	Gly		
	335		340		345
Ile Ser Leu Phe	Leu Ile Ile Ser Met	Cys Leu Leu Phe Leu	Trp		
	350		355		360
Lys Lys Tyr Gln	Pro Tyr Lys Val Ile	Lys Gln Lys Leu Glu	Gly		
	365		370		375
Arg Pro Glu Thr	Glu Tyr Arg Lys Ala	Gln Thr Phe Ser Gly	His		
	380		385		390
Glu Asp Ala Leu	Asp Asp Phe Gly Ile	Tyr Glu Phe Val Ala	Phe		
	395		400		405
Pro Asp Val Ser	Gly Val Ser Arg Ile	Pro Ser Arg Ser Val	Pro		
	410		415		420
Ala Ser Asp Cys	Val Ser Gly Gln Asp	Leu His Ser Thr Val	Tyr		
	425		430		435
Glu Val Ile Gln	His Ile Pro Ala Gln	Gln Gln Asp His Pro	Glu		
	440		445		450

&lt;210&gt; 321

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 321

gatcctgtca caaagccagt ggtgc 25

&lt;210&gt; 322

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 322

cactgacagg gttcctcacc cagg 24

&lt;210&gt; 323

&lt;211&gt; 45

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

0906320.071801

<220>

<223> Synthetic Oligonucleotide Probe

<400> 323

ctccctctgg gctgtggagt atgtggggaa catgaccctg acatg 45

<210> 324

<211> 2397

<212> DNA

<213> Homo Sapien

<400> 324

gcaagcggcg aaatggcgcc ctccgggagt cttgcagttc ccctggcagt 50  
 cctggtgctg ttgctttggg gtgctccctg gacgcacggg cggcggagca 100  
 acgttcgcgt catcacggac gagaactgga gagaactgct ggaaggagac 150  
 tggatgatag aattttatgc cccgtgggtgc cctgcttgct aaaatcttca 200  
 accggaatgg gaaagttttg ctgaatgggg agaagatctt gaggttaata 250  
 ttgcgaaagt agatgtcaca gagcagccag gactgagtgg acggtttatc 300  
 ataactgctc ttcctactat ttatcattgt aaagatgggt aatttaggcg 350  
 ctatcagggg ccaaggacta agaaggactt cataaacttt ataagtgata 400  
 aagagtggaa gagtattgag cccgtttcat catggtttgg tccaggttct 450  
 gttctgatga gtagtatgtc agcactcttt cagctatcta tgtggatcag 500  
 gacgtgccat aactacttta ttgaagacct tggattgcca gtgtggggat 550  
 catatactgt ttttgcttta gcaactctgt tttccggact gttattagga 600  
 ctctgtatga tatttggtggc agattgcctt tgtccttcaa aaaggcgcag 650  
 accacagcca taccataacc cttcaaaaaa attattatca gaatctgcac 700  
 aacctttgaa aaaagtggag gaggaacaag aggcggatga agaagatgtt 750  
 tcagaagaag aagctgaaag taaagaagga acaaacaag actttccaca 800  
 gaatgccata agacaacgct ctctgggtcc atcattggcc acagataaat 850  
 cctagttaaa ttttatagtt atcttaatat tatgatcttg ataaaaacag 900  
 aagattgatc attttggttg gtttgaagtg aactgtgact tttttgaata 950  
 ttgcaggggt cagtctagat tgtcattaaa ttgaagagtc tacattcaga 1000

0990920.0101

acataaaaagc actaggtata caagtttgaa atatgattta agcacagtat 1050  
 gatgggttaa atagttctct aatttttgaa aaatcgtgcc aagcaataag 1100  
 atttatgtat atttgtttaa taataaccta tttcaagtct gagttttgaa 1150  
 aatttacatt tccaagtat tgcattattg aggtatttaa gaagattatt 1200  
 ttagagaaaa atatttctca tttgatataa ttttctctg tttcactgtg 1250  
 tgaaaaaaag aagatatttc ccataaatgg gaagtttgcc cattgtctca 1300  
 agaaatgtgt atttcagtga caatttcgtg gtcttttttag aggtatattc 1350  
 caaaatttcc ttgtattttt aggttatgca actaataaaa actaccttac 1400  
 attaattaat tacagttttc tacacatggg aatacaggat atgctactga 1450  
 tttaggaagt ttttaagttc atggattctt cttgattcca acaaagtttg 1500  
 attttctctt gtatttttct tacttactat ggggttacatt ttttattttt 1550  
 caaattggat gataatttct tggaaacatt ttttatgttt tagtaaacag 1600  
 tatttttttg ttgtttcaaa ctgaagttta ctgagagatc catcaaattg 1650  
 aacaatctgt tgtaatttaa aattttggcc acttttttca gatttttacat 1700  
 cattcttgct gaacttcaac ttgaaattgt ttttttttcc tttttggatg 1750  
 tgaaggtgaa cattcctgat ttttgtctga tgtgaaaaag ccttggtatt 1800  
 ttacattttg aaaattcaaa gaagcttaat ataaaagttt gcattctact 1850  
 caggaaaaag catcttcttg tatatgtctt aaatgtattt ttgtcctcat 1900  
 atacagaaag ttcttaattg attttacagt ctgtaatgct tgatgtttta 1950  
 aaataataac atttttatat tttttaaaag acaaacttca tattatcctg 2000  
 tgttctttcc tgactggtaa tattgtgtgg gatttcacag gtaaaagtca 2050  
 gtaggatgga acatttttagt gtattttttac tccttaaaga gctagaatac 2100  
 atagttttca ccttaaaaga agggggaaaa tcataaatac aatgaatcaa 2150  
 ctgaccatta cgtagtagac aatttctgta atgtccctt ctttctaggc 2200  
 tctgttgctg tgtgaatcca ttagatttac agtatcgtaa tatacaagtt 2250  
 ttctttaaag ccctctcctt tagaatttaa aatattgtac cattaaagag 2300  
 tttggatgtg taacttgtga tgccttagaa aaatatccta agcacaaaat 2350

Met	Ala	Pro	Ser	Gly	Ser	Leu	Ala	Val	Pro	Leu	Ala	Val	Leu	Val
1				5					10					15
Leu	Leu	Leu	Trp	Gly	Ala	Pro	Trp	Thr	His	Gly	Arg	Arg	Ser	Asn
				20					25					30
Val	Arg	Val	Ile	Thr	Asp	Glu	Asn	Trp	Arg	Glu	Leu	Leu	Glu	Gly
				35					40					45
Asp	Trp	Met	Ile	Glu	Phe	Tyr	Ala	Pro	Trp	Cys	Pro	Ala	Cys	Gln
				50					55					60
Asn	Leu	Gln	Pro	Glu	Trp	Glu	Ser	Phe	Ala	Glu	Trp	Gly	Glu	Asp
				65					70					75
Leu	Glu	Val	Asn	Ile	Ala	Lys	Val	Asp	Val	Thr	Glu	Gln	Pro	Gly
				80					85					90
Leu	Ser	Gly	Arg	Phe	Ile	Ile	Thr	Ala	Leu	Pro	Thr	Ile	Tyr	His
				95					100					105
Cys	Lys	Asp	Gly	Glu	Phe	Arg	Arg	Tyr	Gln	Gly	Pro	Arg	Thr	Lys
				110					115					120
Lys	Asp	Phe	Ile	Asn	Phe	Ile	Ser	Asp	Lys	Glu	Trp	Lys	Ser	Ile
				125					130					135
Glu	Pro	Val	Ser	Ser	Trp	Phe	Gly	Pro	Gly	Ser	Val	Leu	Met	Ser
				140					145					150
Ser	Met	Ser	Ala	Leu	Phe	Gln	Leu	Ser	Met	Trp	Ile	Arg	Thr	Cys
				155					160					165
His	Asn	Tyr	Phe	Ile	Glu	Asp	Leu	Gly	Leu	Pro	Val	Trp	Gly	Ser
				170					175					180
Tyr	Thr	Val	Phe	Ala	Leu	Ala	Thr	Leu	Phe	Ser	Gly	Leu	Leu	Leu
				185					190					195
Gly	Leu	Cys	Met	Ile	Phe	Val	Ala	Asp	Cys	Leu	Cys	Pro	Ser	Lys
				200					205					210
Arg	Arg	Arg	Pro	Gln	Pro	Tyr	Pro	Tyr	Pro	Ser	Lys	Lys	Leu	Leu

	215		220		225									
Ser	Glu	Ser	Ala	Gln	Pro	Leu	Lys	Lys	Val	Glu	Glu	Glu	Gln	Glu
	230								235					240
Ala	Asp	Glu	Glu	Asp	Val	Ser	Glu	Glu	Glu	Ala	Glu	Ser	Lys	Glu
	245								250					255
Gly	Thr	Asn	Lys	Asp	Phe	Pro	Gln	Asn	Ala	Ile	Arg	Gln	Arg	Ser
	260								265					270
Leu	Gly	Pro	Ser	Leu	Ala	Thr	Asp	Lys	Ser					
	275								280					

&lt;210&gt; 326

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 326

tgaggtgggc aagcggcgaa atg 23

&lt;210&gt; 327

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 327

tatgtggatc aggacgtgcc 20

&lt;210&gt; 328

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 328

tgcagggttc agtctagatt g 21

&lt;210&gt; 329

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

T08T20"07E0660

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 329  
 ttgaaggaca aaggcaatct gccac 25

<210> 330  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 330  
 ggagtcttgc agttcccttg gcagtcctgg tgetgttgc ttggg 45

<210> 331  
 <211> 2168  
 <212> DNA  
 <213> Homo Sapien

<400> 331  
 gcgagtgtcc agctgaggag acccgtgata attcggtaac taattcaaca 50  
 aacgggaccc ttctgtgtgc cagaaaccgc aagcagttgc taaccagtg 100  
 ggacaggcgg attggaagag cgggaaggtc ctggcccaga gcagtgtgac 150  
 acttccctct gtgaccatga aactctgggt gtctgcattg ctgatggcct 200  
 ggtttggtgt cctgagctgt gtgcaggccg aattcttcac ctctattggg 250  
 cacatgactg acctgattta tgcagagaaa gagctggtgc agtctctgaa 300  
 agagtacatc cttgtggagg aagccaagct ttccaagatt aagagctggg 350  
 ccaacaaaat ggaagccttg actagcaagt cagctgctga tgctgagggc 400  
 tacctggctc accctgtgaa tgctacaaa ctgggtgaagc ggctaaacac 450  
 agactggcct gcgctggagg accttgtcct gcaggactca gctgcagggt 500  
 ttatcgccaa cctctctgtg cagcggcagt tcttccccac tgatgaggac 550  
 gagataggag ctgcccgaagc cctgatgaga cttcaggaca catacaggct 600  
 ggaccagggc acaatttcca gaggggaact tccaggaacc aagtaccagg 650  
 caatgctgag tgtggatgac tgctttggga tgggccgctc ggctacaat 700  
 gaaggggact attatcatatc ggtgttgttg atggagcagg tgctaaagca 750



gcttgatgcc ggggaggagg ccaccacaac caagtcacag gtgctggact 800  
 acctcagcta tgctgtcttc cagttgggtg atctgcaccg tgccctggag 850  
 ctcacccgcc gctgtctctc ccttgacca agccacgaac gagctggagg 900  
 gaatctgagg tactttgagc agttattgga ggaagagaga gaaaaaacgt 950  
 taacaaatca gacagaagct gagctagcaa cccagaagg catctatgag 1000  
 aggctgtgg actacctgcc tgagagggat gtttacgaga gcctctgtcg 1050  
 tggggagggt gtcaaactga cccccgtag acagaagagg cttttctgta 1100  
 ggtaccacca tggcaacagg gccccacagc tgetcattgc ccccttcaaa 1150  
 gaggaggacg agtgggacag cccgcacatc gtcagggtact acgatgtcat 1200  
 gtctgatgag gaaatcgaga ggatcaagga gatcgcaaaa cctaaacttg 1250  
 cacgagccac cgttcgtgat cccaagacag gagtcctcac tgtcgccagc 1300  
 taccgggttt ccaaaagctc ctggctagag gaagatgatg accctgttgt 1350  
 ggcccgagta aatcgtcgga tgcagcatat cacagggtta acagtaaaga 1400  
 ctgcagaatt gttacagggt gcaaattatg gagtgggagg acagtatgaa 1450  
 ccgcacttcg acttctctag gcgacctttt gacagcggcc tcaaacacaga 1500  
 ggggaatagg ttagegacgt ttcttaacta catgagtgat gtagaagctg 1550  
 gtggtgccac cgtcttccct gatctggggg ctgcaatttg gcctaagaag 1600  
 ggtacagctg tgttctggta caacctcttg cggagcgggg aaggtagacta 1650  
 ccgaacaaga catgtgcct gccctgtgct tgtgggctgc aagtgggtct 1700  
 ccaataagtg gttccatgaa cgaggacagg agttcttgag accttgtgga 1750  
 tcaacagaag ttgactgaca tccttttctg tccttcccct tcctggctct 1800  
 tcagcccatg tcaacgtgac agacaccttt gtatgttcct ttgtatgttc 1850  
 ctatcaggct gatTTTTTgga gaaatgaatg tttgtctgga gcagagggag 1900  
 accatactag ggcgactcct gtgtgactga agtcccagcc cttccattca 1950  
 gcctgtgcc tccctggccc caaggctagg atcaaagtgg ctgcagcaga 2000  
 gttagctgtc tagcgcttag caagggtgcct ttgtacctca ggtgttttag 2050  
 gtgtgagatg tttcagtga ccaaagttct gataccttgt ttacatgttt 2100

gtttttatgg catttctatc tattgtggct ttaccaaaaa ataaaatgtc 2150

cctaccagaa aaaaaaaaa 2168

<210> 332

<211> 533

<212> PRT

<213> Homo Sapien

<400> 332

Met Lys Leu Trp Val Ser Ala Leu Leu Met Ala Trp Phe Gly Val  
1 5 10 15

Leu Ser Cys Val Gln Ala Glu Phe Phe Thr Ser Ile Gly His Met  
20 25 30

Thr Asp Leu Ile Tyr Ala Glu Lys Glu Leu Val Gln Ser Leu Lys  
35 40 45

Glu Tyr Ile Leu Val Glu Glu Ala Lys Leu Ser Lys Ile Lys Ser  
50 55 60

Trp Ala Asn Lys Met Glu Ala Leu Thr Ser Lys Ser Ala Ala Asp  
65 70 75

Ala Glu Gly Tyr Leu Ala His Pro Val Asn Ala Tyr Lys Leu Val  
80 85 90

Lys Arg Leu Asn Thr Asp Trp Pro Ala Leu Glu Asp Leu Val Leu  
95 100 105

Gln Asp Ser Ala Ala Gly Phe Ile Ala Asn Leu Ser Val Gln Arg  
110 115 120

Gln Phe Phe Pro Thr Asp Glu Asp Glu Ile Gly Ala Ala Lys Ala  
125 130 135

Leu Met Arg Leu Gln Asp Thr Tyr Arg Leu Asp Pro Gly Thr Ile  
140 145 150

Ser Arg Gly Glu Leu Pro Gly Thr Lys Tyr Gln Ala Met Leu Ser  
155 160 165

Val Asp Asp Cys Phe Gly Met Gly Arg Ser Ala Tyr Asn Glu Gly  
170 175 180

Asp Tyr Tyr His Thr Val Leu Trp Met Glu Gln Val Leu Lys Gln  
185 190 195

Leu Asp Ala Gly Glu Glu Ala Thr Thr Thr Lys Ser Gln Val Leu  
200 205 210

09909320.071801

Asp Tyr Leu Ser	Tyr Ala Val Phe Gln Leu Gly Asp Leu His Arg	215	220	225
Ala Leu Glu Leu	Thr Arg Arg Leu Leu Ser Leu Asp Pro Ser His	230	235	240
Glu Arg Ala Gly	Gly Asn Leu Arg Tyr Phe Glu Gln Leu Leu Glu	245	250	255
Glu Glu Arg Glu	Lys Thr Leu Thr Asn Gln Thr Glu Ala Glu Leu	260	265	270
Ala Thr Pro Glu	Gly Ile Tyr Glu Arg Pro Val Asp Tyr Leu Pro	275	280	285
Glu Arg Asp Val	Tyr Glu Ser Leu Cys Arg Gly Glu Gly Val Lys	290	295	300
Leu Thr Pro Arg	Arg Gln Lys Arg Leu Phe Cys Arg Tyr His His	305	310	315
Gly Asn Arg Ala	Pro Gln Leu Leu Ile Ala Pro Phe Lys Glu Glu	320	325	330
Asp Glu Trp Asp	Ser Pro His Ile Val Arg Tyr Tyr Asp Val Met	335	340	345
Ser Asp Glu Glu	Ile Glu Arg Ile Lys Glu Ile Ala Lys Pro Lys	350	355	360
Leu Ala Arg Ala	Thr Val Arg Asp Pro Lys Thr Gly Val Leu Thr	365	370	375
Val Ala Ser Tyr	Arg Val Ser Lys Ser Ser Trp Leu Glu Glu Asp	380	385	390
Asp Asp Pro Val	Val Ala Arg Val Asn Arg Arg Met Gln His Ile	395	400	405
Thr Gly Leu Thr	Val Lys Thr Ala Glu Leu Leu Gln Val Ala Asn	410	415	420
Tyr Gly Val Gly	Gly Gln Tyr Glu Pro His Phe Asp Phe Ser Arg	425	430	435
Arg Pro Phe Asp	Ser Gly Leu Lys Thr Glu Gly Asn Arg Leu Ala	440	445	450
Thr Phe Leu Asn	Tyr Met Ser Asp Val Glu Ala Gly Gly Ala Thr	455	460	465
Val Phe Pro Asp	Leu Gly Ala Ala Ile Trp Pro Lys Lys Gly Thr	470	475	480

00909320-071801

Ala Val Phe Trp Tyr Asn Leu Leu Arg Ser Gly Glu Gly Asp Tyr  
485 490 495

Arg Thr Arg His Ala Ala Cys Pro Val Leu Val Gly Cys Lys Trp  
500 505 510

Val Ser Asn Lys Trp Phe His Glu Arg Gly Gln Glu Phe Leu Arg  
515 520 525

Pro Cys Gly Ser Thr Glu Val Asp  
530

<210> 333

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 333

ccaggcacaa tttccaga 18

<210> 334

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 334

ggacccttct gtgtgccag 19

<210> 335

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 335

ggtctcaaga actcctgtc 19

<210> 336

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

09909320.071801

<400> 336  
acactcagca ttgcctggta cttg 24

<210> 337

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 337

gggcacatga ctgacctgat ttatgcagag aaagagctgg tgcag 45

<210> 338

<211> 2789

<212> DNA

<213> Homo Sapien

<400> 338

gcagattga gttttacttc ctctctttt tagtgaaga cagaccataa 50  
tcccagtgtg agtgaaattg attgtttcat ttattaccgt tttggctggg 100  
ggtagttcc gacaccttca cagtgaaga gcaggcagaa ggagttgtga 150  
agacaggaca atcttcttgg ggatgctggg cctggaagcc agcgggcctt 200  
gctctgtctt tggcctcatt gaccccaggt tctctggta aaactgaaag 250  
cctactactg gcctggtgcc catcaatcca ttgatccttg aggctgtgcc 300  
cctggggcac ccacctggca gggcctacca ccatgcgact gagctccctg 350  
ttggctctgc tgcggccagc gcttcccctc atcttagggc tgtctctggg 400  
gtgcagcctg agcctcctgc gggtttcctg gatccagggg gagggagaag 450  
atccctgtgt cgaggctgta ggggagcgag gagggccaca gaatccagat 500  
tcgagagctc ggctagacca aagtgatgaa gacttcaaac cccggattgt 550  
cccctactac agggacccca acaagcccta caagaagggtg ctcaggactc 600  
ggtacatcca gacagagctg ggctcccctg agcggttgct ggtggctgtc 650  
ctgacctccc gagctacact gtccactttg gccgtggctg tgaaccgtac 700  
ggtggcccat cacttccctc ggttactcta cttcactggg cagcgggggg 750  
cccgggctcc agcagggatg caggtggtgt ctcatgggga tgagcgggcc 800

gcctggctca tgtcagagac cctgcgccac cttcacacac actttggggc 850  
 cgactacgac tggttcttca tcatgcagga tgacacatat gtgcaggccc 900  
 cccgcctggc agcccttgct ggccacctca gcatcaacca agacctgtac 950  
 ttaggccggg cagaggagtt cattggcgca ggcgagcagg cccggtactg 1000  
 tcatgggggc tttggctacc tgttgtcacg gagtctcctg cttcgtctgc 1050  
 ggccacatct ggatggctgc cgaggagaca ttctcagtgc ccgtcctgac 1100  
 gagtggcttg gacgctgcct cattgactct ctgggcgtcg gctgtgtctc 1150  
 acagcaccag gggcagcagt atcgctcatt tgaactggcc aaaaataggg 1200  
 accctgagaa ggaagggagc tcggctttcc tgagtgcctt cgccgtgcac 1250  
 cctgtctccg aaggtagcct catgtaccgg ctccacaaac gcttcagcgc 1300  
 tctggagttg gagcgggctt acagtgaat agaacaactg caggctcaga 1350  
 tccggaacct gaccgtgctg acccccgaag gggaggcagg gctgagctgg 1400  
 cccgttgggc tccctgctcc tttcacacca cactctcgtt ttgaggtgct 1450  
 gggctgggac tacttcacag agcagcacac cttctcctgt gcagatgggg 1500  
 ctcccaagtg cccactacag ggggctagca gggcggacgt gggatgatgcg 1550  
 ttggagactg ccctggagca gctcaatcgg cgctatcagc cccgcctgcg 1600  
 cttccagaag cagcgactgc tcaacggcta tcggcgcttc gaccagcac 1650  
 ggggcatgga gtacaccctg gacctgctgt tggaatgtgt gacacagcgt 1700  
 gggcacggc gggccctggc tcgcagggtc agcctgctgc ggccactgag 1750  
 ccgggtggaa atcctaccta tgccctatgt cactgaggcc acccgagtgc 1800  
 agctgggtgct gccactcctg gtggctgaag ctgctgcagc cccggctttc 1850  
 ctcgaggcgt ttgcagccaa tgtcctggag ccacgagaac atgcattgct 1900  
 caccctgttg ctggtctacg ggccacgaga aggtggccgt ggagctccag 1950  
 acccatttct tgggggtgaag gctgcagcag cggagttaga gcgacggtac 2000  
 cctgggacga ggctggcctg gctcgctgtg cgagcagagg ccccttccca 2050  
 ggtgcgactc atggacgtgg tctcgaagaa gcaccctgtg gacactctct 2100

09909320.071801

```
<210> 339
<211> 772
<212> PRT
<213> Homo Sapien
```

Met	Arg	Leu	Ser	Ser	Leu	Leu	Ala	Leu	Leu	Arg	Pro	Ala	Leu	Pro
1				5					10					15
Leu	Ile	Leu	Gly	Leu	Ser	Leu	Gly	Cys	Ser	Leu	Ser	Leu	Leu	Arg
				20					25					30
Val	Ser	Trp	Ile	Gln	Gly	Glu	Gly	Glu	Asp	Pro	Cys	Val	Glu	Ala
				35					40					45
Val	Gly	Glu	Arg	Gly	Gly	Pro	Gln	Asn	Pro	Asp	Ser	Arg	Ala	Arg
				50					55					60
Leu	Asp	Gln	Ser	Asp	Glu	Asp	Phe	Lys	Pro	Arg	Ile	Val	Pro	Tyr
				65					70					75
Tyr	Arg	Asp	Pro	Asn	Lys	Pro	Tyr	Lys	Lys	Val	Leu	Arg	Thr	Arg
				80					85					90
Tyr	Ile	Gln	Thr	Glu	Leu	Gly	Ser	Arg	Glu	Arg	Leu	Leu	Val	Ala

	95		100		105
Val Leu Thr Ser	Arg Ala Thr Leu Ser	Thr Leu Ala Val	Ala Val		
	110		115		120
Asn Arg Thr Val	Ala His His Phe Pro	Arg Leu Leu Tyr	Phe Thr		
	125		130		135
Gly Gln Arg Gly	Ala Arg Ala Pro Ala	Gly Met Gln Val	Val Ser		
	140		145		150
His Gly Asp Glu	Arg Pro Ala Trp Leu	Met Ser Glu Thr	Leu Arg		
	155		160		165
His Leu His Thr	His Phe Gly Ala Asp	Tyr Asp Trp Phe	Phe Ile		
	170		175		180
Met Gln Asp Asp	Thr Tyr Val Gln Ala	Pro Arg Leu Ala	Ala Leu		
	185		190		195
Ala Gly His Leu	Ser Ile Asn Gln Asp	Leu Tyr Leu Gly	Arg Ala		
	200		205		210
Glu Glu Phe Ile	Gly Ala Gly Glu Gln	Ala Arg Tyr Cys	His Gly		
	215		220		225
Gly Phe Gly Tyr	Leu Leu Ser Arg Ser	Leu Leu Leu Arg	Leu Arg		
	230		235		240
Pro His Leu Asp	Gly Cys Arg Gly Asp	Ile Leu Ser Ala	Arg Pro		
	245		250		255
Asp Glu Trp Leu	Gly Arg Cys Leu Ile	Asp Ser Leu Gly	Val Gly		
	260		265		270
Cys Val Ser Gln	His Gln Gly Gln Gln	Tyr Arg Ser Phe	Glu Leu		
	275		280		285
Ala Lys Asn Arg	Asp Pro Glu Lys Glu	Gly Ser Ser Ala	Phe Leu		
	290		295		300
Ser Ala Phe Ala	Val His Pro Val Ser	Glu Gly Thr Leu	Met Tyr		
	305		310		315
Arg Leu His Lys	Arg Phe Ser Ala Leu	Glu Leu Glu Arg	Ala Tyr		
	320		325		330
Ser Glu Ile Glu	Gln Leu Gln Ala Gln	Ile Arg Asn Leu	Thr Val		
	335		340		345
Leu Thr Pro Glu	Gly Glu Ala Gly Leu	Ser Trp Pro Val	Gly Leu		
	350		355		360

09509320.071801



Pro	Ala	Pro	Phe	Thr	Pro	His	Ser	Arg	Phe	Glu	Val	Leu	Gly	Trp	
				365					370					375	
Asp	Tyr	Phe	Thr	Glu	Gln	His	Thr	Phe	Ser	Cys	Ala	Asp	Gly	Ala	
				380					385					390	
Pro	Lys	Cys	Pro	Leu	Gln	Gly	Ala	Ser	Arg	Ala	Asp	Val	Gly	Asp	
				395					400					405	
Ala	Leu	Glu	Thr	Ala	Leu	Glu	Gln	Leu	Asn	Arg	Arg	Tyr	Gln	Pro	
				410					415					420	
Arg	Leu	Arg	Phe	Gln	Lys	Gln	Arg	Leu	Leu	Asn	Gly	Tyr	Arg	Arg	
				425					430					435	
Phe	Asp	Pro	Ala	Arg	Gly	Met	Glu	Tyr	Thr	Leu	Asp	Leu	Leu	Leu	
				440					445					450	
Glu	Cys	Val	Thr	Gln	Arg	Gly	His	Arg	Arg	Ala	Leu	Ala	Arg	Arg	
				455					460					465	
Val	Ser	Leu	Leu	Arg	Pro	Leu	Ser	Arg	Val	Glu	Ile	Leu	Pro	Met	
				470					475					480	
Pro	Tyr	Val	Thr	Glu	Ala	Thr	Arg	Val	Gln	Leu	Val	Leu	Pro	Leu	
				485					490					495	
Leu	Val	Ala	Glu	Ala	Ala	Ala	Ala	Pro	Ala	Phe	Leu	Glu	Ala	Phe	
				500					505					510	
Ala	Ala	Asn	Val	Leu	Glu	Pro	Arg	Glu	His	Ala	Leu	Leu	Thr	Leu	
				515					520					525	
Leu	Leu	Val	Tyr	Gly	Pro	Arg	Glu	Gly	Gly	Arg	Gly	Ala	Pro	Asp	
				530					535					540	
Pro	Phe	Leu	Gly	Val	Lys	Ala	Ala	Ala	Ala	Glu	Leu	Glu	Arg	Arg	
				545					550					555	
Tyr	Pro	Gly	Thr	Arg	Leu	Ala	Trp	Leu	Ala	Val	Arg	Ala	Glu	Ala	
				560					565					570	
Pro	Ser	Gln	Val	Arg	Leu	Met	Asp	Val	Val	Ser	Lys	Lys	His	Pro	
				575					580					585	
Val	Asp	Thr	Leu	Phe	Phe	Leu	Thr	Thr	Val	Trp	Thr	Arg	Pro	Gly	
				590					595					600	
Pro	Glu	Val	Leu	Asn	Arg	Cys	Arg	Met	Asn	Ala	Ile	Ser	Gly	Trp	
				605					610					615	
Gln	Ala	Phe	Phe	Pro	Val	His	Phe	Gln	Glu	Phe	Asn	Pro	Ala	Leu	
				620					625					630	

FOR 20" 02E6060

Ser Pro Gln Arg Ser Pro Pro Gly Pro Pro Gly Ala Gly Pro Asp  
 635 640 645  
 Pro Pro Ser Pro Pro Gly Ala Asp Pro Ser Arg Gly Ala Pro Ile  
 650 655 660  
 Gly Gly Arg Phe Asp Arg Gln Ala Ser Ala Glu Gly Cys Phe Tyr  
 665 670 675  
 Asn Ala Asp Tyr Leu Ala Ala Arg Ala Arg Leu Ala Gly Glu Leu  
 680 685 690  
 Ala Gly Gln Glu Glu Glu Glu Ala Leu Glu Gly Leu Glu Val Met  
 695 700 705  
 Asp Val Phe Leu Arg Phe Ser Gly Leu His Leu Phe Arg Ala Val  
 710 715 720  
 Glu Pro Gly Leu Val Gln Lys Phe Ser Leu Arg Asp Cys Ser Pro  
 725 730 735  
 Arg Leu Ser Glu Glu Leu Tyr His Arg Cys Arg Leu Ser Asn Leu  
 740 745 750  
 Glu Gly Leu Gly Gly Arg Ala Gln Leu Ala Met Ala Leu Phe Glu  
 755 760 765  
 Gln Glu Gln Ala Asn Ser Thr  
 770

<210> 340

<211> 1572

<212> DNA

<213> Homo Sapien

<400> 340

cggagtgggtg cgccaacgtg agaggaaaacc cgtgcgcggc tgcgctttcc 50  
 tgtccccaag ccgttctaga cgcgggaaaa atgctttctg aaagcagctc 100  
 ctttttgaag ggtgtgatgc ttggaagcat tttctgtgct ttgatcacta 150  
 tgctaggaca cattaggatt ggtcatggaa atagaatgca ccaccatgag 200  
 catcatcacc tacaagctcc taacaaagaa gatatcttga aaatttcaga 250  
 ggatgagcgc atggagctca gtaagagctt tcgagtatac tgtattatcc 300  
 ttgtaaaacc caaagatgtg agtctttggg ctgcagtaaa ggagacttgg 350  
 accaaacact gtgacaaagc agagttcttc agttctgaaa atgttaaagt 400

gtttgagtca attaatatgg acacaaatga catgtgggta atgatgagaa 450  
 aagcttaciaa atacgccttt gataagtata gagaccaata caactgggtc 500  
 ttccttgcaac gcccactac gtttgctatc attgaaaacc taaagtattt 550  
 tttgttaaaa aaggatccat cacagccttt ctatctaggc cacactataa 600  
 aatctggaga ccttgaatat gtgggtatgg aaggaggaat tgtcttaagt 650  
 gtagaatcaa tgaaaagact taacagcctt ctcaatatcc cagaaaagtg 700  
 tcctgaacag ggagggatga tttggaagat atctgaagat aaacagctag 750  
 cagtttgcct gaaatatgct ggagtatttg cagaaaatgc agaagatgct 800  
 gatggaaaag atgtatttaa taccaaatct gttgggcttt ctattaaaga 850  
 ggcaatgact tatcacccca accaggtagt agaaggctgt tgttcagata 900  
 tggetgttac ttttaatgga ctgactccaa atcagatgca tgtgatgatg 950  
 tatgggggtat accgccttag ggcatttggg catattttca atgatgcatt 1000  
 ggtttttctta cctccaaatg gttctgacaa tgactgagaa gtggtagaaa 1050  
 agcgtgaata tgatctttgt ataggacgtg tgttgtcatt atttgtagta 1100  
 gtaactacat atccaatata gctgtatggt tctttttctt ttctaatttg 1150  
 gtggcactgg tataaccaca cattaaagtc agtagtacat ttttaaatga 1200  
 ggggtggtttt tttctttaaa acacatgaac attgtaaatg tgttggaaaag 1250  
 aagtgtttta agaataataa ttttgcaa atactattaa taaatattat 1300  
 atgtgataaa ttctaaatta tgaacattag aaatctgtgg ggcacatatt 1350  
 tttgctgatt gggttaaaaaa ttttaacagg tcttttagcgt tctaagatat 1400  
 gcaaatgata tctctagttg tgaatttgtg attaaagtaa aacttttagc 1450  
 tgtgtgttcc ctttacttct aatactgatt tatgttctaa gcctcccaa 1500  
 gttccaatgg atttgccttc tcaaaatgta caactaagca actaaagaaa 1550  
 attaaagtga aagttgaaaa at 1572

<210> 341

<211> 318

<212> PRT

<213> Homo Sapien

0909320.071801

&lt;400&gt; 341

Met	Leu	Ser	Glu	Ser	Ser	Ser	Phe	Leu	Lys	Gly	Val	Met	Leu	Gly	1	5	10	15
Ser	Ile	Phe	Cys	Ala	Leu	Ile	Thr	Met	Leu	Gly	His	Ile	Arg	Ile	20	25	30	
Gly	His	Gly	Asn	Arg	Met	His	His	His	Glu	His	His	His	Leu	Gln	35	40	45	
Ala	Pro	Asn	Lys	Glu	Asp	Ile	Leu	Lys	Ile	Ser	Glu	Asp	Glu	Arg	50	55	60	
Met	Glu	Leu	Ser	Lys	Ser	Phe	Arg	Val	Tyr	Cys	Ile	Ile	Leu	Val	65	70	75	
Lys	Pro	Lys	Asp	Val	Ser	Leu	Trp	Ala	Ala	Val	Lys	Glu	Thr	Trp	80	85	90	
Thr	Lys	His	Cys	Asp	Lys	Ala	Glu	Phe	Phe	Ser	Ser	Glu	Asn	Val	95	100	105	
Lys	Val	Phe	Glu	Ser	Ile	Asn	Met	Asp	Thr	Asn	Asp	Met	Trp	Leu	110	115	120	
Met	Met	Arg	Lys	Ala	Tyr	Lys	Tyr	Ala	Phe	Asp	Lys	Tyr	Arg	Asp	125	130	135	
Gln	Tyr	Asn	Trp	Phe	Phe	Leu	Ala	Arg	Pro	Thr	Thr	Phe	Ala	Ile	140	145	150	
Ile	Glu	Asn	Leu	Lys	Tyr	Phe	Leu	Leu	Lys	Lys	Asp	Pro	Ser	Gln	155	160	165	
Pro	Phe	Tyr	Leu	Gly	His	Thr	Ile	Lys	Ser	Gly	Asp	Leu	Glu	Tyr	170	175	180	
Val	Gly	Met	Glu	Gly	Gly	Ile	Val	Leu	Ser	Val	Glu	Ser	Met	Lys	185	190	195	
Arg	Leu	Asn	Ser	Leu	Leu	Asn	Ile	Pro	Glu	Lys	Cys	Pro	Glu	Gln	200	205	210	
Gly	Gly	Met	Ile	Trp	Lys	Ile	Ser	Glu	Asp	Lys	Gln	Leu	Ala	Val	215	220	225	
Cys	Leu	Lys	Tyr	Ala	Gly	Val	Phe	Ala	Glu	Asn	Ala	Glu	Asp	Ala	230	235	240	
Asp	Gly	Lys	Asp	Val	Phe	Asn	Thr	Lys	Ser	Val	Gly	Leu	Ser	Ile	245	250	255	
Lys	Glu	Ala	Met	Thr	Tyr	His	Pro	Asn	Gln	Val	Val	Glu	Gly	Cys				

FOR 20-02E60660

	260		265		270
Cys Ser Asp Met	Ala Val Thr Phe Asn Gly Leu Thr Pro Asn Gln				
	275		280		285
Met His Val Met	Met Tyr Gly Val Tyr Arg Leu Arg Ala Phe Gly				
	290		295		300
His Ile Phe Asn Asp Ala Leu Val Phe Leu Pro Pro Asn Gly Ser					
	305		310		315

Asp Asn Asp

<210> 342

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 342

tccccaagcc gttctagacg cgg 23

<210> 343

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 343

ctgggtcttc cttgcacg 18

<210> 344

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 344

gcccaaatgc cctaaggcgg tatacccc 28

<210> 345

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

FOR 20" OF 6060

<223> Synthetic Oligonucleotide Probe

<400> 345

gggtgtgatg cttggaagca ttttctgtgc ttgatcact atgctaggac 50

<210> 346

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 346

gggatgcagg tgggtgtctca tgggg 25

<210> 347

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 347

ccctcatgta ccggctcc 18

<210> 348

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 348

ggattctaatac gactcact atagggctca gaaaagcgca acagagaa 48

<210> 349

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 349

ctatgaaatt aacctcact aaagggatgt cttccatgcc aaccttc 47

<210> 350

<211> 48

<212> DNA

<213> Artificial Sequence

059030-01301

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 350  
ggattctaatacgcactcactatagggcgccgatgtccactggggctac48

<210> 351  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 351  
ctatgaaattaacccctcactaaagggacgaggaagatggcggatggg48

<210> 352  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 352  
ggattctaatacgcactcactatagggcaccacgcgtccggctgctt47

<210> 353  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 353  
ctatgaaattaacccctcactaaagggacggggacaccacggaccaga48

<210> 354  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 354  
ggattctaatacgcactcactatagggcttgctgcggttttgttcctg48

<210> 355  
<211> 48

F08F70-02E50660

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 355  
ctatgaaatt aaccctcact aaaggagct gccgatccca ctggtatt 48

<210> 356  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 356  
ggattctaatacgcactcact atagggcgga tcctggccgg cctctg 46

<210> 357  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 357  
ctatgaaatt aaccctcact aaaggagcc cgggcatggt ctcagtta 48

<210> 358  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 358  
ggattctaatacgcactcact atagggcggg aagatggcga ggaggag 47

<210> 359  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 359  
ctatgaaatt aaccctcact aaaggaccca aggccacaaa cggaatc 48

T08T/0"02E50660



<210> 360  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 360  
ggattctaatac gactcact atagggctgt gctttcattc tgccagta 48

<210> 361  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 361  
ctatgaaatt aaccctcact aaaggaggagg tacaattaag gggaggat 48

<210> 362  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 362  
ggattctaatac gactcact atagggcccg cctcgctcct gctcctg 47

<210> 363  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 363  
ctatgaaatt aaccctcact aaaggaggagg ttgccgcgac cctcacag 48

<210> 364  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 364



<223> Synthetic Oligonucleotide Probe

<400> 369

ctatgaaatt aaccctcact aaagggaaag acatgtcatc gggagtgg 48

<210> 370

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 370

ggattctaatacgcactcact atagggccgg gtggaggtgg aacagaaa 48

<210> 371

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 371

ctatgaaatt aaccctcact aaagggacac agacagagcc ccatacgc 48

<210> 372

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 372

ggattctaatacgcactcact atagggccag ggaaatccgg atgtctc 47

<210> 373

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 373

ctatgaaatt aaccctcact aaagggagta aggggatgcc accgagta 48

<210> 374

<211> 47

<212> DNA

<213> Artificial Sequence

FOR "0" DE 60660

<220>

<223> Synthetic Oligonucleotide Probe

<400> 374

ggattctaatac gactcact atagggccag ctacccgcag gaggagg 47

<210> 375

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 375

ctatgaaatt aacctcact aaagggatcc caggtgatga ggtccaga 48

<210> 376

<211> 997

<212> DNA

<213> Homo Sapien

<400> 376

cccacgcgtc cgatcttacc aacaaaacac tcctgaggag aaagaaagag 50

agggagggag agaaaaagag agagagagaa acaaaaaacc aaagagagag 100

aaaaaatgaa ttcattctaaa tcattctgaaa cacaatgcac agagagagga 150

tgtttctctt cccaaatggt cttatggact gttgctggga tccccatcct 200

atttctcagt gctgttttca tcaccagatg tggttgagaca tttcgcattc 250

ttcaaacctg tgatgagaaa aagtttcagc tacctgagaa tttcacagag 300

ctctcctgct acaattatgg atcagggttca gtcaagaatt gttgtccatt 350

gaactgggaa tattttcaat ccagctgcta cttcttttct actgacacca 400

tttctctggc gttaagttaa aagaactgct cagccatggg ggctcacctg 450

gtggttatca actcacagga ggagcaggaa ttcctttcct acaagaaacc 500

taaaatgaga gagtttttta ttggactgtc agaccagggt gtcgagggtc 550

agtggcaatg ggtggacggc acacctttga caaagtctct gagcttcttg 600

gatgtagggg agcccaacaa catagctacc ctggaggact gtgccaccat 650

gagagactct tcaaacccaa ggcaaaattg gaatgatgta acctgtttcc 700

tcaattatct tcggatttgt gaaatggtag gaataaatcc tttgaacaaa 750

09909330.071301

ggaaaatctc tttaagaaca gaaggcacaa ctcaaattgtg taaagaagga 800  
 agagcaagaa catggccaca cccaccgccc cacacgagaa atttgtgcgc 850  
 tgaacttcaa aggacttcat aagtatttgt tactctgata caaataaaaa 900  
 taagtagttt taaatgttaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 950  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 997

<210> 377

<211> 219

<212> PRT

<213> Homo Sapien

<400> 377

Met	Asn	Ser	Ser	Lys	Ser	Ser	Glu	Thr	Gln	Cys	Thr	Glu	Arg	Gly	1	5	10	15
Cys	Phe	Ser	Ser	Gln	Met	Phe	Leu	Trp	Thr	Val	Ala	Gly	Ile	Pro	20	25	30	
Ile	Leu	Phe	Leu	Ser	Ala	Cys	Phe	Ile	Thr	Arg	Cys	Val	Val	Thr	35	40	45	
Phe	Arg	Ile	Phe	Gln	Thr	Cys	Asp	Glu	Lys	Lys	Phe	Gln	Leu	Pro	50	55	60	
Glu	Asn	Phe	Thr	Glu	Leu	Ser	Cys	Tyr	Asn	Tyr	Gly	Ser	Gly	Ser	65	70	75	
Val	Lys	Asn	Cys	Cys	Pro	Leu	Asn	Trp	Glu	Tyr	Phe	Gln	Ser	Ser	80	85	90	
Cys	Tyr	Phe	Phe	Ser	Thr	Asp	Thr	Ile	Ser	Trp	Ala	Leu	Ser	Leu	95	100	105	
Lys	Asn	Cys	Ser	Ala	Met	Gly	Ala	His	Leu	Val	Val	Ile	Asn	Ser	110	115	120	
Gln	Glu	Glu	Gln	Glu	Phe	Leu	Ser	Tyr	Lys	Lys	Pro	Lys	Met	Arg	125	130	135	
Glu	Phe	Phe	Ile	Gly	Leu	Ser	Asp	Gln	Val	Val	Glu	Gly	Gln	Trp	140	145	150	
Gln	Trp	Val	Asp	Gly	Thr	Pro	Leu	Thr	Lys	Ser	Leu	Ser	Phe	Trp	155	160	165	
Asp	Val	Gly	Glu	Pro	Asn	Asn	Ile	Ala	Thr	Leu	Glu	Asp	Cys	Ala	170	175	180	

09909320.074301

Thr Met Arg Asp Ser Ser Asn Pro Arg Gln Asn Trp Asn Asp Val  
                           185                          190                          195

Thr Cys Phe Leu Asn Tyr Phe Arg Ile Cys Glu Met Val Gly Ile  
                           200                          205                          210

Asn Pro Leu Asn Lys Gly Lys Ser Leu  
                           215

<210> 378

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 378

ttcagcttct gggatgtagg g 21

<210> 379

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 379

tattcctacc atttcacaaa tccg 24

<210> 380

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 380

ggaggactgt gccacatga gagactcttc aaaccaagg caaaattgg 49

<210> 381

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 381

gcagattttg aggacagcca cctcca 26

09909320.071801

<210> 382  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 382  
ggccttgag acaaccgt 18

<210> 383  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 383  
cagactgagg gagatccgag a 21

<210> 384  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 384  
cagctgccct tccccaacca 20

<210> 385  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 385  
catcaagcgc ctctacca 18

<210> 386  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 386

cacaaactcg aactgcttct g 21

<210> 387

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 387

gggccatcac agctccct 18

<210> 388

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 388

gggatgtggt gaacacagaa ca 22

<210> 389

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 389

tgccagctgc atgctgccag tt 22

<210> 390

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 390

cagaaggatg tcccgtggaa 20

<210> 391

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

FOR 20" 03E50660



<223> Synthetic oligonucleotide probe

<400> 391

gccgctgtcc actgcag 17

<210> 392

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 392

gacggcatcc tcagggccac a 21

<210> 393

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 393

atgtcctcca tgcccacgcg 20

<210> 394

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 394

gagtgcgaca tcgagagctt 20

<210> 395

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 395

ccgcagcctc agtgatga 18

<210> 396

<211> 21

<212> DNA

<213> Artificial Sequence

FOBT20"02E60660

<220>  
<223> Synthetic oligonucleotide probe

<400> 396  
gaagagcaca gctgcagatc c 21

<210> 397  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 397  
gaggtgtcct ggctttggtg gt 22

<210> 398  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 398  
cctctggcgc cccactcaa 20

<210> 399  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 399  
ccaggagagc tggcgatg 18

<210> 400  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 400  
gcaaattcag ggctcactag aga 23

<210> 401  
<211> 29

FOR "02060660"

<212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 401  
     cacagagcat ttgtccatca gcagttcag 29  
  
 <210> 402  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 402  
     ggcagagact tccagtcact ga 22  
  
 <210> 403  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 403  
     gccaaagggtg gtgtagata gg 22  
  
 <210> 404  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 404  
     caggccccct tgatctgtac ccca 24  
  
 <210> 405  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 405  
     gggacgtgct tctacaagaa cag 23

090923.0130  
 02E60660

<210> 406  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 406  
caggcttaca atggttatgat cagaca 26

<210> 407  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 407  
tattcagagt tttccattgg cagtgccagt t 31

<210> 408  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 408  
tctacatcag cctctctgcg c 21

<210> 409  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 409  
cgatcttctc caccaggag cgg 23

<210> 410  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 410

gccaggcctc acattcgt 18

<210> 411

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 411

ctccctgaat ggcagcctga gca 23

<210> 412

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 412

aggtgtttat taagggccta cgct 24

<210> 413

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 413

cagagcagag ggtgccttg 19

<210> 414

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 414

tggcggagtc ccctcttggc t 21

<210> 415

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

090920.07101

<223> Synthetic oligonucleotide probe

<400> 415

ccctgtttcc ctatgcatca ct 22

<210> 416

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 416

tcaaccctg accctttcct a 21

<210> 417

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 417

ggcaggggac aagccatctc tcct 24

<210> 418

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 418

gggactgaac tgccagcttc 20

<210> 419

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 419

gggccctaac ctcattacct tt 22

<210> 420

<211> 23

<212> DNA

<213> Artificial Sequence

FOBT/0"02E60660

<220>

<223> Synthetic oligonucleotide probe

<400> 420

tgtctgcctc agccccagga agg 23

<210> 421

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 421

tctgtccacc atcttgcctt g 21

<210> 422

<211> 3554

<212> DNA

<213> Homo Sapien

<400> 422

gggactacaa gccgcgcgc gctgccgctg gcccctcagc aaccctcgac 50  
 atggcgctga ggcggccacc gcgactccgg ctctgcgctc ggctgcctga 100  
 cttcttctctg ctgctgcttt tcaggggctg cctgataggg gctgtaaatc 150  
 tcaaattccag caatcgaacc ccagtggtag aggaatttga aagtgtggaa 200  
 ctgtcttgca tcattacgga ttcgcagaca agtgacccca ggatcgagtg 250  
 gaagaaaatt caagatgaac aaaccacata tgtgtttttt gacaacaaaa 300  
 ttcaggggaga cttggcgggt cgtgcagaaa tactggggaa gacatccctg 350  
 aagatctgga atgtgacacg gagagactca gccctttatc gctgtgaggt 400  
 cgttgctcga aatgaccgca aggaaattga tgagatttg atcgagttaa 450  
 ctgtgcaagt gaagccagt acccctgtct gtagagtgc gaaggctgta 500  
 ccagtaggca agatggcaac actgcactgc caggagagtg agggccaccc 550  
 ccggcctcac tacagctgg atcgcaatga tgtaccactg cccacggatt 600  
 ccagagccaa tcccagattt cgcaattctt ctttccactt aaactctgaa 650  
 acaggcactt tgggtgtcac tgctgttcac aaggacgact ctgggcagta 700  
 ctactgcatt gcttccaatg acgcaggctc agccagggtg gaggagcagg 750

09909320-071801

agatggaagt ctatgacctg aacattggcg gaattattgg gggggttctg 800  
 gttgtccttg ctgtactggc cctgatcacg ttgggcatct gctgtgcata 850  
 cagacgtggc tacttcatca acaataaaca ggatggagaa agttacaaga 900  
 acccagggaa accagatgga gttaactaca tccgcactga cgaggagggc 950  
 gacttcagac acaagtcacg gtttgtgatc tgagacccgc ggtgtggctg 1000  
 agagcgcaca gagcgcacgt gcacatacct ctgctagaaa ctctgtcaa 1050  
 ggcagcgaga gctgatgcac tcggacagag ctagacactc attcagaagc 1100  
 ttttcgtttt ggccaaagtt gaccactact cttcttactc taacaagcca 1150  
 catgaataga agaattttcc tcaagatgga cccggtaaat ataaccacaa 1200  
 ggaagcgaaa ctgggtgcgt tcaactgagtt gggttcctaa tctgtttctg 1250  
 gcctgattcc cgcattgagta ttagggatgat cttaaagagt ttgctcacgt 1300  
 aaacgcccgt gctgggccct gtgaagccag catgttcacc actggctggt 1350  
 cagcagccac gacagcacca tgtgagatgg cgagggtggc ggacagcacc 1400  
 agcagcgcac cccggcgga acccagaaaa ggcttcttac acagcagcct 1450  
 tacttcatcg gccacagac accaccgcag tttcttctta aaggctctgc 1500  
 tgatcggtgt tgcagtgtcc attgtggaga agctttttgg atcagcattt 1550  
 tgtaaaaaca accaaaatca ggaaggtaaa ttggttgctg gaagagggat 1600  
 cttgcctgag gaacctgct tgtccaacag ggtgtcagga ttttaaggaaa 1650  
 accttcgtct taggctaagt ctgaaatggc actgaaatat gcttttctat 1700  
 gggctctggt tattttataa aattttacat cttaaatttt gctaaggatg 1750  
 tattttgatt attgaaaaga aaatttctat ttaaactgta aatatattgt 1800  
 catacaatgt taaataacct atttttttaa aaaagttcaa cttaaggtag 1850  
 aagttccaag ctactagtgt taaattggaa aatatcaata attaagagta 1900  
 ttttacccaa ggaatcctct catggaagtt tactgtgatg ttctttttct 1950  
 cacacaagtt ttagcctttt tcacaaggga actcatactg tctacacatc 2000  
 agaccatagt tgcttaggaa acctttaaaa attccagtta agcaatggtg 2050

09909320-071801



aaatcagttt gcatctcttc aaaagaaacc tctcaggtta gctttgaact 2100  
 gcctcttctt gagatgacta ggacagtctg taccagagg ccaccagaa 2150  
 gccctcagat gtacatacac agatgccagt cagctcctgg ggttgcgcca 2200  
 ggcgcccccg ctctagctca ctggtgcctc gctgtctgcc aggaggccct 2250  
 gccatccttg ggccctggca gtggctgtgt ccagtgagc tttactcacg 2300  
 tggcccttgc ttcattccagc acagctctca ggtgggcact gcagggacac 2350  
 tgggtgtcttc catgtagcgt ccagctttg ggctcctgta acagacctct 2400  
 ttttggttat ggatggctca caaaataggg ccccaatgc ttttttttt 2450  
 ttttaagttt gtttaattat ttgttaagat tgtctaaggc caaaggcaat 2500  
 tgcgaaatca agtctgtcaa gtacaataac atttttaaaa gaaaatggat 2550  
 cccactgttc ctctttgcc aagagaaagc acccagacgc cacaggctct 2600  
 gtcgcatttc aaaacaaacc atgatggagt ggcggccagt ccagcctttt 2650  
 aaagaacgtc aggtggagca gccaggtgaa aggcctggcg gggaggaaaag 2700  
 tgaaacgcct gaatcaaaag cagttttcta attttgactt taaatttttc 2750  
 atccgcgga gacactgttc ccatttgtgg ggggacatta gcaacatcac 2800  
 tcagaagcct gtgttcttca agagcaggtg ttctcagcct cacatgccct 2850  
 gccgtgctgg actcaggact gaagtgtgt aaagcaagga gctgctgaga 2900  
 aggagcactc cactgtgtgc ctggagaatg gctctcacta ctcaccttgt 2950  
 ctttcagctt ccagtgtctt gggtttttta tactttgaca gctttttttt 3000  
 aattgcatac atgagactgt gttgactttt tttagttagt tgaaacactt 3050  
 tgccgcaggc cgctggcag aggcaggaaa tgctccagca gtggctcagt 3100  
 gctccctggg gtctgtgca tggcatcctg gatgcttagc atgcaagttc 3150  
 cctccatcat tgccaccttg gtagagaggg atggctcccc accctcagcg 3200  
 ttggggattc acgtccagc ctcttcttgg gttgtcatag tgatagggtta 3250  
 gccttattgc cccctcttct tataacctaa aacctctac actagtgccca 3300  
 tgggaaccag gtctgaaaaa gtagagagaa gtgaaagtag agtctgggaa 3350  
 gtagctgcct ataactgaga ctagacggaa aaggaatact cgtgtatttt 3400

0909320-071801

090930-071803

<400> 423														
Met	Ala	Leu	Arg	Arg	Pro	Pro	Arg	Leu	Arg	Leu	Cys	Ala	Arg	Leu
1				5					10					15
Pro	Asp	Phe	Phe	Leu	Leu	Leu	Leu	Phe	Arg	Gly	Cys	Leu	Ile	Gly
				20					25					30
Ala	Val	Asn	Leu	Lys	Ser	Ser	Asn	Arg	Thr	Pro	Val	Val	Gln	Glu
				35					40					45
Phe	Glu	Ser	Val	Glu	Leu	Ser	Cys	Ile	Ile	Thr	Asp	Ser	Gln	Thr
				50					55					60
Ser	Asp	Pro	Arg	Ile	Glu	Trp	Lys	Lys	Ile	Gln	Asp	Glu	Gln	Thr
				65					70					75
Thr	Tyr	Val	Phe	Phe	Asp	Asn	Lys	Ile	Gln	Gly	Asp	Leu	Ala	Gly
				80					85					90
Arg	Ala	Glu	Ile	Leu	Gly	Lys	Thr	Ser	Leu	Lys	Ile	Trp	Asn	Val
				95					100					105
Thr	Arg	Arg	Asp	Ser	Ala	Leu	Tyr	Arg	Cys	Glu	Val	Val	Ala	Arg
				110					115					120
Asn	Asp	Arg	Lys	Glu	Ile	Asp	Glu	Ile	Val	Ile	Glu	Leu	Thr	Val
				125					130					135
Gln	Val	Lys	Pro	Val	Thr	Pro	Val	Cys	Arg	Val	Pro	Lys	Ala	Val
				140					145					150
Pro	Val	Gly	Lys	Met	Ala	Thr	Leu	His	Cys	Gln	Glu	Ser	Glu	Gly
				155					160					165
His	Pro	Arg	Pro	His	Tyr	Ser	Trp	Tyr	Arg	Asn	Asp	Val	Pro	Leu
				170					175					180
Pro	Thr	Asp	Ser	Arg	Ala	Asn	Pro	Arg	Phe	Arg	Asn	Ser	Ser	Phe
				185					190					195

His	Leu	Asn	Ser	Glu	Thr	Gly	Thr	Leu	Val	Phe	Thr	Ala	Val	His
				200					205					210
Lys	Asp	Asp	Ser	Gly	Gln	Tyr	Tyr	Cys	Ile	Ala	Ser	Asn	Asp	Ala
				215					220					225
Gly	Ser	Ala	Arg	Cys	Glu	Glu	Gln	Glu	Met	Glu	Val	Tyr	Asp	Leu
				230					235					240
Asn	Ile	Gly	Gly	Ile	Ile	Gly	Gly	Val	Leu	Val	Val	Leu	Ala	Val
				245					250					255
Leu	Ala	Leu	Ile	Thr	Leu	Gly	Ile	Cys	Cys	Ala	Tyr	Arg	Arg	Gly
				260					265					270
Tyr	Phe	Ile	Asn	Asn	Lys	Gln	Asp	Gly	Glu	Ser	Tyr	Lys	Asn	Pro
				275					280					285
Gly	Lys	Pro	Asp	Gly	Val	Asn	Tyr	Ile	Arg	Thr	Asp	Glu	Glu	Gly
				290					295					300
Asp	Phe	Arg	His	Lys	Ser	Ser	Phe	Val	Ile					
				305					310					

0909320.071801